


```
CC Revised record issued on 09-SEP-2004 : Correction to Organism field
XX Sequence 421 AA:
SQ Query Match 100.0%; Score 2290; DB 4; Length 421;
Best Local Similarity 100.0%; Pred. No. 4,4e-185;
Matches 421; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGRGPAAGSARRPPPLP-LTLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLIATCS 60
DB 1 MPAGRGPAAGSARRPPPLP-LTLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLIATCS 60
QY 61 VHGDPGATAGLTYWTINGRRLLPELSRVYLNASTLALANLNGSRSGDNLVCHARDG 120
DB 61 VHGDPGATAGLTYWTINGRRLLPELSRVYLNASTLALANLNGSRSGDNLVCHARDG 120
QY 121 SIILAGSCLYVGLPPEKPVNISCSKMKDILTCRWTPGAHGETFLHTNYSILKTKLRWYGO 180
DB 121 SIILAGSCLYVGLPPEKPVNISCSKMKDILTCRWTPGAHGETFLHTNYSILKTKLRWYGO 180
QY 181 NTCEBYHTVGPBHSCHI PKDIALFTPYEITWEATNRLGSARSDVLTLDILDVYTTDPPDY 240
DB 181 NTCEBYHTVGPBHSCHI PKDIALFTPYEITWEATNRLGSARSDVLTLDILDVYTTDPPDY 240
QY 241 HVSRVGLIEDQLSVRWVSPALDKFLFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGL 300
DB 241 HVSRVGLIEDQLSVRWVSPALDKFLFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGL 300
QY 301 KPGTYVYVQVRCNPFYIGSKKAGIWSHPTAASPRSGRPGGACPRGGEPSSG 360
DB 301 KPGTYVYVQVRCNPFYIGSKKAGIWSHPTAASPRSGRPGGACPRGGEPSSG 360
QY 361 PVRRRLKQFLGWLKKAHVCNSLSEFLYDQWRAMWQSKHKTNRNDEGILPSGRGTARGP 420
DB 361 PVRRRLKQFLGWLKKAHVCNSLSEFLYDQWRAMWQSKHKTNRNDEGILPSGRGTARGP 420
QY 421 R 421
DB 421 R 421

RESULT 2
AA05782 standard; protein; 422 AA.
ID AAY05782
AC AAY05782;
XX 02-AUG-1999 (first entry)
DT 02-AUG-1999 (first entry)
DE Human type 1 cytokine receptor GBRI-ILR.
XX GBRI-ILR; hGBR-ILR; cytokine receptor; human; cancer; obesity;
XX inflammation; septic shock; AIDS; embryo development; lung infection;
XX cytoskeletal; anorectic; immunosuppressive; antibacterial; antiviral;
XX antiinflammatory; therapy.
XX Homo sapiens.
OS
XX Key 1..37 Location/Qualifiers
XX FT Peptide /note="signal peptide"
XX FT Protein /note="mature protein; a polypeptide comprising amino
XX acids 38-422 is also claimed in Claim 1a"
XX PN MO9920755-A2.
XX PD 29-APR-1999.
XX PF 14-OCT-1998; 98WO-EP006497.
XX PR 16-OCT-1997; 97GB-00021961.
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XX (GLAXO ) GLAXO GROUP LTD.
PA Elson G, Gauchat J, Kosco-Vilbois M;
XX WPI; 1999-288305/24.
XX N-PSDB; AAX25489.
XX Novel human or mouse type I cytokine receptors hGBRI-ILR or mGBRI-ILR,
XX useful for treating e.g. cancer, immune disorders, obesity and AIDS.
XX Claim 1a; Fig 4; 41pp; English.
XX The present sequence represents a novel type 1 cytokine receptor that has
XX been termed human GBRI-ILR as it is believed to be an interleukin
XX receptor, or at least a substantial part of such a receptor. The sequence
XX is predicted from an isolated full-length cDNA clone (see AAX25489)
XX obtained from a human placental cDNA library. GBRI-ILR mRNA is expressed
XX most strongly in spleen, thymus, lymph node, appendix, bone marrow,
XX thymoid, adrenal cortex, stomach, heart, placenta and skeletal muscle,
XX suggesting a role for GBRI-ILR in the immune system. In human foetal
XX tissue, strong expression is seen in the lung, but not in brain, kidney
XX or liver. A GBRI-ILR receptor has also been identified in mice (see
XX AAY05783). The high degree of conservation of amino acids between the
XX human and murine polypeptides indicates that this receptor is
XX functionally important. GBRI-ILR polypeptides, nucleic acids, antibodies,
XX agonists and antagonists can be used to treat e.g. cancer, immune
XX disorders, obesity (in view of homology to the leptin receptor),
XX embryonic developmental disorders, AIDS, septic shock and lung infection
XX (claimed)
XX Sequence 422 AA;
SQ Query Match 99.5%; Score 2279.5; DB 2; Length 422;
Best Local Similarity 99.8%; Pred. No. 3,4e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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QY 1 MPAGRGPAAGSARRPPPLP-LTLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLIATC 59
DB 1 MPAGRGPAAGSARRPPPLP-LTLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLIATC 60
QY 60 VHGDPGATAGLTYWTINGRRLLPELSRVYLNASTLALANLNGSRSGDNLVCHARD 119
DB 61 VHGDPGATAGLTYWTINGRRLLPELSRVYLNASTLALANLNGSRSGDNLVCHARD 120
QY 120 GSILAGSCLYVGLPPEKPVNISCSKMKDILTCRWTPGAHGETFLHTNYSILKTKLRWYGO 179
DB 121 GSILAGSCLYVGLPPEKPVNISCSKMKDILTCRWTPGAHGETFLHTNYSILKTKLRWYGO 180
QY 180 DMTCEBYHTVGPBHSCHI PKDIALFTPYEITWEATNRLGSARSDVLTLDILDVYTTDPPD 239
DB 181 DMTCEBYHTVGPBHSCHI PKDIALFTPYEITWEATNRLGSARSDVLTLDILDVYTTDPPD 240
QY 240 VHSRVGLIEDQLSVRWVSPALDKFLFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGL 299
DB 241 VHSRVGLIEDQLSVRWVSPALDKFLFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGL 300
QY 300 LKPGTYVYVQVRCNPFYIGSKKAGIWSHPTAASPRSGRPGGACPRGGEPSS 359
DB 301 LKPGTYVYVQVRCNPFYIGSKKAGIWSHPTAASPRSGRPGGACPRGGEPSS 360
QY 360 GPVRRRLKQFLGWLKKAHVCNSLSEFLYDQWRAMWQSKHKTNRNDEGILPSGRGTARGP 419
DB 361 GPVRRRLKQFLGWLKKAHVCNSLSEFLYDQWRAMWQSKHKTNRNDEGILPSGRGTARGP 420
QY 420 AR 421
DB 421 AR 422

RESULT 3
AA06479 standard; protein; 422 AA.
ID AAY06479
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XX AA06479;
AC
AC 27-SEP-1999 (first entry)
DT
XX Human tumour-associated protein PRO327.
XX PRO327; UNQ288; cancer; tumour; diagnosis; therapy; human.
XX Homo sapiens.
XX MO9935170-A4.
XX 15-JUL-1999.
XX
XX 05-JAN-1999; 99MO-US000106.
XX
XX 05-JAN-1998/ 98US-0070440P.
XX 29-APR-1998/ 98US-0083500P.
XX 22-MAY-1998/ 98US-0086414P.
XX 10-JUN-1998/ 98US-0088742P.
XX 10-NOV-1998/ 98US-0107783P.
XX 20-NOV-1998/ 98US-0109304P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA, Roy MA;
PI Wood WI;
XX MPI; 1999-430385/36.
XX DR N-PSDB; AAX87256.
XX
XX Anticbody agglutinate proteins expressed in neoplastic cells, useful for tumor
PT diagnosis and treatment.
XX
XX Example 1; Fig 6; 162pp; English.
XX
XX This sequence represents human PRO327 (UNQ288), a 46.3 kDa protein (pI
CC 9.42) encoded by the novel cDNA clone DNA38113 (see AAX87256).
CC Amplification of DNA38113 occurs in various lung and colon tumours and
CC cell lines, suggesting a significant role in tumour formation and growth.
CC Antagonists (e.g. antibodies) directed against PRO327 are expected to
CC have utility in cancer therapy. The invention identifies 14 genes (see
CC AAX87254-67) that are amplified in the genome of tumour cells. Such
CC amplification is expected to be associated with overexpression of the
CC gene product and to contribute to tumorigenesis. The encoded proteins
CC (see AA06477-90) may be useful targets for the diagnosis and/or
CC treatment (including prevention) of certain cancers, and may act as
CC predictors of the prognosis of tumour treatment. Antibodies that bind the
CC proteins are claimed and used in claimed cancer diagnostic kits
CC
XX Sequence 422 AA;
SQ
Query Match 99.5%; Score 2279.5; DB 2; Length 422;
Best Local Similarity 99.8%; Pred. No. 3,4e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLAGAPRAGSAGHTAVISPODPTLLIGSSILATC 59
DB 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLAGAPRAGSAGHTAVISPODPTLLIGSSILATC 60
QY 60 SVHGDPGATAGTGLVMTNLRRLPPELSRTIANSTLALANLNGSRQSGDNLVCHARD 119
DB 61 SVHGDPGATAGTGLVMTNLRRLPPELSRTIANSTLALANLNGSRQSGDNLVCHARD 120
QY 120 GSLLASGLVGLPPEKPVNISCSKMKDLCRTWTPGAGETFLHTNYSLKYLAWYQ 179
DB 121 GSLLASGLVGLPPEKPVNISCSKMKDLCRTWTPGAGETFLHTNYSLKYLAWYQ 180
QY 180 DNTCEHYTVGPSCHIPKDLALFTPYEIVEATNRLGARSVDLTLDLIVVTTDPPD 239
DB 181 DNTCEHYTVGPSCHIPKDLALFTPYEIVEATNRLGARSVDLTLDLIVVTTDPPD 240

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QY 240 VHSRVGLEDQSLVSRVSPALPKDFLQAKYQIRRVEDSVDMKYVDVSNQTSCLAG 299
DB 241 VHSRVGLEDQSLVSRVSPALPKDFLQAKYQIRRVEDSVDMKYVDVSNQTSCLAG 300
QY 300 LKPGTYFVQVRCNPFQIYGSKKAGIWEWSHPTAASPRSEPPGCGACEPRGEPSS 359
DB 301 LKPGTYFVQVRCNPFQIYGSKKAGIWEWSHPTAASPRSEPPGCGACEPRGEPSS 360
QY 360 GPVREIKQFLGMLKKHAYCSNLSFRLYDQWRAMQSKHTRNODGILPSGRGRTARGP 419
DB 361 GPVREIKQFLGMLKKHAYCSNLSFRLYDQWRAMQSKHTRNODGILPSGRGRTARGP 420
QY 420 AR 421
DB 421 AR 422

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RESULT 4
AA017825
ID AA017825 standard; protein; 422 AA.

AA017825;
AC
XX
XX 12-AUG-1999 (first entry)
DT
XX
XX Human PRO327 protein sequence.
DE
XX Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
XX secreted protein; transmembrane protein; inflammation disorder.
XX
XX Homo sapiens.
OS
XX
XX MO9928462-A2.
PN
XX 10-JUN-1999.
PD
XX
XX 01-DEC-1998; 98MO-US025108.
PF
XX
XX 03-DEC-1997; 97US-0067411P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 12-DEC-1997; 97US-0069425P.
PR 16-DEC-1997; 97US-0069594P.
PR 16-DEC-1997; 97US-0069596P.
PR 16-DEC-1997; 97US-0069702P.
PR 17-DEC-1997; 97US-0069870P.
PR 17-DEC-1997; 97US-0069873P.
PR 18-DEC-1997; 97US-0068017P.
PR 05-JAN-1998; 98US-0070440P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-FEB-1998; 98US-0075945P.
XX
XX (GETH) GENENTECH INC.
PA
XX Wood WI, Goddard A, Gurney AL, Yuan J, Baker KP, Chen J;
PI MPI; 1999-371118/31.
XX DR N-PSDB; AAX80050.
XX
XX Nucleic acids encoding PRO secreted and transmembrane proteins.
PT Claim 12; Fig 17; 123pp; English.
XX
XX The present invention describes nucleic acids encoding PRO secreted and
CC transmembrane proteins used therapeutically. The PRO proteins have
CC cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
CC activity. The proteins and polynucleotides can be used in therapy,
CC identification of homologues, raising antibodies and design of probes and
CC primers. They can be used in a range of antibodies related to proteins that
CC they have homology with, e.g. a PRO protein having homology to complement
CC proteins may be used in inflammatory responses

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XX Sequence 422 AA;
SQ Query Match 99.5%; Score 2279.5; DB 2; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.4e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MPAGRRGPAAGSARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSILATC 59
DB 1 MPAGRRGPAAGSARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSILATC 60
QY 60 SVHGDPPGATABGLWYTLNGRRLPELSRVLNASTLALANLNGSRSGDNLVCHARD 119
DB 61 SVHGDPPGATABGLWYTLNGRRLPELSRVLNASTLALANLNGSRSGDNLVCHARD 120
QY 120 GSIIAGSCLYVGLPPEKPVNISGWSKNMKDLTCRWTPGAHGETFLHTNYSLKYLKWYQ 179
DB 121 GSIIAGSCLYVGLPPEKPVNISGWSKNMKDLTCRWTPGAHGETFLHTNYSLKYLKWYQ 180
QY 180 DNTCEHYHTVGPSSCHIPKDLALFTPYEITWVATNRLGSARSDVLTLDLDVVTTPDPD 239
DB 181 DNTCEHYHTVGPSSCHIPKDLALFTPYEITWVATNRLGSARSDVLTLDLDVVTTPDPD 240
QY 240 VHSRVGGLIEDQLSVWVSPPALKDPLFOAKYQIRYVEDSVDMKYVDVSNQTSCLAG 299
DB 241 VHSRVGGLIEDQLSVWVSPPALKDPLFOAKYQIRYVEDSVDMKYVDVSNQTSCLAG 300
QY 300 LKRGTYFVQVRCNPFGIYGSKKAGIWEWSHPTAASPRSRPGGACBPRGGEPS 359
DB 301 LKRGTYFVQVRCNPFGIYGSKKAGIWEWSHPTAASPRSRPGGACBPRGGEPS 360
QY 360 GPRRELKQFLGWLKHAACSNLSFRLYDQWRAWMOKSHKTRNODGILPSGRGTARGP 419
DB 361 GPRRELKQFLGWLKHAACSNLSFRLYDQWRAWMOKSHKTRNODGILPSGRGTARGP 420
QY 420 AR 421
DB 421 AR 422

RESULT 5
AA26339
ID AAY26339 standard; protein; 422 AA.
AC AAY26339;
DT 13-JAN-2000 (first entry)
XX
DE Human U4 haematopoietin receptor superfamily chain-2.
XX
KW Human U4 protein; haematopoietin receptor superfamily;
KW biological activity; cytokine; cell proliferation; cell differentiation;
KW immune stimulation; immune suppression; haematopoiesis regulation;
KW immune disorder; immune deficiency; autoimmune disorder; allergy; cancer;
KW myeloid cell; lymphoid cell deficiency; platelet disorder.
XX
OS Homo sapiens.
XX
PN WO953066-A1.
XX
PD 21-OCT-1999.
XX
PE 09-APR-1999; 99WO-US007882.
XX
PR 10-APR-1998; 98US-00058660.
XX
PA (GEMV ) GENETICS INST INC.
XX
PI Donaldson D, Collins M, Whitters M, Neben T;
XX
DR WPI; 1999-611303/52.
XX
DR N-PSDB; AAX90754.
XX
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PT Novel polypeptides and polynucleotides used for treatment of human
PT diseases and disorders e.g. immune disorders or deficiencies caused by
PT fungal, parasitic or viral infections.
XX
XX Claim 9; Page 36-38; 43pp; English.
XX
PS The present sequence is a human U4 protein which is predicted to have the
CC haematopoietin receptor superfamily. The protein is predicted to have the
CC following biological activities: cytokine, cell
CC proliferation/differentiation, immune stimulating or suppressing and
CC haematopoiesis regulating. The U4 protein can be used to treat immune
CC disorders and deficiencies, autoimmune disorders, allergies, cancer,
CC myeloid or lymphoid cell deficiencies and platelet disorders
XX
SQ Sequence 422 AA;
Query Match 99.5%; Score 2279.5; DB 2; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.4e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MPAGRRGPAAGSARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSILATC 59
DB 1 MPAGRRGPAAGSARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSILATC 60
QY 60 SVHGDPPGATABGLWYTLNGRRLPELSRVLNASTLALANLNGSRSGDNLVCHARD 119
DB 61 SVHGDPPGATABGLWYTLNGRRLPELSRVLNASTLALANLNGSRSGDNLVCHARD 120
QY 120 GSIIAGSCLYVGLPPEKPVNISGWSKNMKDLTCRWTPGAHGETFLHTNYSLKYLKWYQ 179
DB 121 GSIIAGSCLYVGLPPEKPVNISGWSKNMKDLTCRWTPGAHGETFLHTNYSLKYLKWYQ 180
QY 180 DNTCEHYHTVGPSSCHIPKDLALFTPYEITWVATNRLGSARSDVLTLDLDVVTTPDPD 239
DB 181 DNTCEHYHTVGPSSCHIPKDLALFTPYEITWVATNRLGSARSDVLTLDLDVVTTPDPD 240
QY 240 VHSRVGGLIEDQLSVWVSPPALKDPLFOAKYQIRYVEDSVDMKYVDVSNQTSCLAG 299
DB 241 VHSRVGGLIEDQLSVWVSPPALKDPLFOAKYQIRYVEDSVDMKYVDVSNQTSCLAG 300
QY 300 LKRGTYFVQVRCNPFGIYGSKKAGIWEWSHPTAASPRSRPGGACBPRGGEPS 359
DB 301 LKRGTYFVQVRCNPFGIYGSKKAGIWEWSHPTAASPRSRPGGACBPRGGEPS 360
QY 360 GPRRELKQFLGWLKHAACSNLSFRLYDQWRAWMOKSHKTRNODGILPSGRGTARGP 419
DB 361 GPRRELKQFLGWLKHAACSNLSFRLYDQWRAWMOKSHKTRNODGILPSGRGTARGP 420
QY 420 AR 421
DB 421 AR 422

RESULT 6
AAB01316
ID AAB01316 standard; protein; 422 AA.
AC AAB01316;
DT 25-SEP-2000 (first entry)
XX
DE Human PRO327 polypeptide.
XX
KW PRO, membrane bound protein; secreted protein; PRO357; PRO243;
KW PRO715; PRO241; PRO323; PRO299; PRO344; PRO347; PRO355; PRO353;
KW PRO361; PRO365; transmembrane polypeptide; antibody; screening;
KW detection; inhibition; probe; primer; human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT 1..30
XX FT /label=Signal peptide
```


FT	Modified-site	3. .7	/note= "Amidation site"
FT	Modified-site	30. .36	/note= "N-myristoylation site"
FT	Modified-site	37. .43	/note= "N-myristoylation site"
FT	Modified-site	44. .61	/note= "N-myristoylation site"
FT	Domain	/label=	Transmembrane domain
FT	Modified-site	73. .79	/note= "N-myristoylation site"
FT	Modified-site	79. .83	/note= "Amidation site"
FT	Modified-site	92. .96	/note= "N-glycosylation site"
FT	Modified-site	104. .108	/note= "N-glycosylation site"
FT	Modified-site	121. .127	/note= "N-myristoylation site"
FT	Modified-site	140. .144	/note= "N-glycosylation site"
FT	Modified-site	168. .172	/note= "N-glycosylation site"
FT	Modified-site	179. .185	/note= "N-myristoylation site"
FT	Modified-site	218. .224	/note= "N-myristoylation site"
FT	Modified-site	292. .296	/note= "N-glycosylation site"
FT	Modified-site	300. .306	/note= "N-myristoylation site"
FT	Modified-site	317. .323	/note= "N-myristoylation site"
FT	Modified-site	320. .326	/note= "N-myristoylation site"
FT	Modified-site	325. .331	/label= Growth factor/cytokine receptor family signature
FT	Modified-site	347. .353	/note= "N-myristoylation site"
FT	Modified-site	355. .361	/note= "N-myristoylation site"
FT	Modified-site	382. .386	/note= "N-glycosylation site"
FT	Modified-site	407. .413	/note= "N-myristoylation site"
FT	Modified-site	413. .417	/note= "cAMP and cGMP-dependent protein kinase phosphorylation site"
PN	W0200032776-A2.		
XX	08-JUN-2000.		
XX	01-DEC-1999;	99WO-US028301.	
XX	01-DEC-1998;	98WO-US025108.	
XX	16-DEC-1998;	98US-0112850P.	
XX	22-DEC-1998;	98US-0113296P.	
PA	(GETH) GENENTECH INC.		
XX	Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E,		
PI	Gerlitsen ME, Goddard A, Godowski PJ, Grimaldi CU, Gurney AU,		
PI	Hillan KJ, Kljgvin ID, Napier MA, Roy MA, Tumas D, Wood WI;		
DR	WPI: 2000-412324/35.		
XX	N-PSDB; AAA49558.		
XX	New human nucleic acids encoding secreted and transmembrane polypeptides		
PT	designated as PRO polypeptides, useful as pharmaceutical and diagnostic		
XX	agents.		
XX	Claim 12; Fig 14; 187pp; English.		

CC	New human nuclear acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides and are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources	
CC	XX	Sequence 422 AA;
CC	XX	Query Match 99.5%; Score 2279.5; DB 3; Length 422; Best Local Similarity 99.8%; Pred. No. 3.4e-184; Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
CC	QY	1 MPAGRRPAAQASARRPPLLP-LLLLCVLGAPRAGSANTAVISPQDPTLLIGSSLATC 59
CC	Db	1 MPAGRRPAAQASARRPPLLP-LLLLCVLGAPRAGSANTAVISPQDPTLLIGSSLATC 60
CC	QY	60 SVHGDPGATAEGLIYTLNGRRLLPPELSRYLNASTLALANLNGSRQSGDNLYCHARD 119
CC	Db	61 SVHGDPGATAEGLIYTLNGRRLLPPELSRYLNASTLALANLNGSRQSGDNLYCHARD 120
CC	QY	120 GSILAGSLYVGLPPEKPVNISCSKMKDLCRTWPGAGGFELHNNYSIKYLRMYGQ 179
CC	Db	121 GSILAGSLYVGLPPEKPVNISCSKMKDLCRTWPGAGGFELHNNYSIKYLRMYGQ 180
CC	QY	180 DNTCEEHATVGPSPHSCHLPKDLALFTPYEIVEATNRLGARSVDLTLDIDVYTTDPPD 239
CC	Db	181 DNTCEEHATVGPSPHSCHLPKDLALFTPYEIVEATNRLGARSVDLTLDIDVYTTDPPD 240
CC	QY	240 VHSVRVGLDEDLQSLSVRVSPPALKDLFLQAKYQIRYVEDSDMKVVDVDSNGTSCRLAG 299
CC	Db	241 VHSVRVGLDEDLQSLSVRVSPPALKDLFLQAKYQIRYVEDSDMKVVDVDSNGTSCRLAG 300
CC	QY	300 LKPEYTVFVQVRCNPGFIVGSKAGIWEKSHPTAATPSERPGCGACERPGERSS 359
CC	Db	301 LKPEYTVFVQVRCNPGFIVGSKAGIWEKSHPTAATPSERPGCGACERPGERSS 360
CC	QY	360 GPVARELKQFLGMLKKAIVCSNLSFRLYDDQRAWMQSKHTRNDDEGILPSGRGRTARGP 419
CC	Db	361 GPVARELKQFLGMLKKAIVCSNLSFRLYDDQRAWMQSKHTRNDDEGILPSGRGRTARGP 420
CC	QY	420 AR 421
CC	Db	421 AR 422
CC	XX	RESULT 7
CC	XX	AAV93686
CC	XX	AAV93686 standard; protein; 422 AA.
CC	XX	AAV93686;
CC	XX	03-OCT-2000 (first entry)
CC	XX	Amino acid sequence of novel polypeptide PRO327.
CC	XX	PRO201; PRO3292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumor cell; tumorigenesis; cancer; neoplastic cell growth; cell proliferation.
CC	XX	Homo sapiens.
CC	XX	Location/Qualifiers
CC	XX	1..30
CC	XX	/note= "signal sequence"
CC	XX	3..7
CC	XX	/note= "amidation site"
CC	XX	30..36
CC	XX	/note= "N-myristoylation site"
CC	XX	37..43
CC	XX	/note= "N-myristoylation site"

PT	Modified-site	44..48	
PT	/note= "casein kinase II phosphorylation site"		
FT	Modified-site	73..79	
FT	/note= "N-myristoylation site"		
FT	Modified-site	79..83	
FT	/note= "amidation site"		
FT	Modified-site	92..96	
FT	/note= "N-glycosylation site"		
FT	Modified-site	104..108	
FT	/note= "N-glycosylation site"		
FT	Modified-site	121..127	
FT	/note= "N-myristoylation site"		
FT	Modified-site	140..144	
FT	/note= "N-glycosylation site"		
FT	Modified-site	168..172	
FT	/note= "N-glycosylation site"		
FT	Modified-site	179..185	
FT	/note= "N-myristoylation site"		
FT	Modified-site	183..187	
FT	/note= "casein kinase II phosphorylation site"		
FT	Modified-site	205..209	
FT	/note= "casein kinase II phosphorylation site"		
FT	Modified-site	218..224	
FT	/note= "N-myristoylation site"		
FT	Modified-site	292..296	
FT	/note= "N-glycosylation site"		
FT	Modified-site	300..306	
FT	/note= "N-myristoylation site"		
FT	Modified-site	317..323	
FT	/note= "N-myristoylation site"		
FT	Modified-site	320..326	
FT	/note= "N-myristoylation site"		
FT	Modified-site	325..332	
FT	/note= "Growth factor and cytokines receptor family signature 2"		
FT	Modified-site	347..353	
FT	/note= "N-myristoylation site"		
FT	Modified-site	355..361	
FT	/note= "N-myristoylation site"		
FT	Modified-site	382..386	
FT	/note= "N-glycosylation site"		
FT	Modified-site	407..413	
FT	/note= "N-myristoylation site"		
FT	Modified-site	411..415	
FT	/note= "amidation site"		
FT	Modified-site	413..417	
FT	/note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"		
XX			
PN	WO200037640-A2.		
XX			
PD	29-JUN-2000.		
XX			
PF	16-DEC-1999;		
XX			
XX	99WO-US030095.		
XX			
XX	22-DEC-1998;		
PR	98US-0113296P.		
PR	08-MAR-1999;		
PR	99WO-US005028.		
PR	02-JUN-1999;		
PR	99WO-US012252.		
PR	01-SEP-1999;		
PR	99WO-US020111.		
PR	15-SEP-1999;		
PR	99WO-US021090.		
PR	30-NOV-1999;		
PR	99WO-US028313.		
PR	30-NOV-1999;		
PR	99WO-US028409.		
PR	01-DEC-1999;		
PR	99WO-US028301.		
PR	02-DEC-1999;		
XX	99WO-US028565.		
XX			
PA	(GETH) GENENTECH INC.		
XX			
PI	Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA,		
XX	Wood WI;		
XX			
XX	WPI, 2000-452188/39.		
DR	N-PSDB; AAA46902.		
XX			

PT New anti-polypeptide antibody useful in the treatment and diagnosis of
PT neoplastic cell growth and proliferation.
XX
XX
PS Claim 61; Fig 6; 220pp; English.
XX
CC The present sequence describes a novel human polypeptide. The
CC specification describes novel polypeptides designated PRO201, PRO292,
CC PRO327, PRO1265, PRO344, PRO343, PRO347, PRO357, PRO715, PRO1011,
CC PRO1112, PRO3509, PRO853 and PRO882. These genes are amplified in the
CC genome of tumour cells. The polypeptides are believed to contribute to
CC tumorigenesis. The polypeptides are useful target for the identification
CC of certain cancers, and may act as predictors of the prognosis of tumour
CC treatment. Antibodies against these polypeptides are useful in the
CC treatment and diagnosis of neoplastic cell growth and proliferation in
CC mammals
XX
SQ Sequence 422 AA;

Query Match	99.5%	Score 2279.5;	DB 3;	length 422;
Best Local Similarity	99.8%;	Pred. No. 3.4e-184;		
Matches 421; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1.

QY 1 MPAGRGPAAGSARRPPPLP-LILLCTLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 59
DB 1 MPAGRGGAAGSARRPPPLP-LILLCTLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60

QY 60 SYHGDPPGATAGEGLWYTLNGRRLLPEELSRVLTASTLALANLANSRQRSGNVLCHARD 119
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 SYHGDPPEATAGEGLWYTLNGRRLLPEELSRVLTASTLALANLANSRQRSGNVLCHARD 120

QY 120 GSILAGSCLYVGLPEPEKPVNISCSKKNKMDLTCRMTPGAHGTFPLHTVYSLKCYKLRYGQ 179
121 GSILAGSCLYVGLPEPEKPVNISCSKKNKMDLTCRMTPGAHGTFPLHTVYSLKCYKLRYGQ 180

Oy	180 DNTCEEHTVGNHSHIPIKDLAFTPYEHWEA TNRIGARSVDLTLDLIVVTTPDPED	239
Dib	181 DNTCEEHTVGHSCHIPKDALTFPYEHWEA TNRIGARSVDLTLDLIVVTTPDPED	240

Qy 240 VAVSRVGGIEDOLSVRWSPPALKFLPOAKYQIRYVEDSVDMKVVDDVSNQTSRLAG 299

Db 241 VAVSRVGGIEDOLSVRWSPPALKFLPOAKYQIRYVEDSVDMKVVDDVSNQTSRLAG 300

QY 300 LKPGTVYFVQVACNPFGIYGSKKAGIWSMWSHPPLASTRSTRSRPRPGGGACCPRGSGPS 359
301 LKPGTVYFVQVACNPFGIYGSKKAGIWSMWSHPPLASTRSTRSRPRPGGGACCPRGSGPS 360
DB

QY	360	GEVRBELKQFLGMLKKHAYCSNLSRFLYDQMPANQKSKHTN	ODEGII	PSGRGTARGE	419
DB	361	GEVRBELKQFLGMLKKHAYCSNLSRFLYDQMPANQKSKHTN	ODEGII	PSGRGTARGE	420

QY	420 AR 421
DB	421 AR 422

RESULT 8
AA63545

ID	AMG63545 standard; protein; 422 AA.
XX	
XX	
AC	AMG63545;
XX	
XX	

DT 15-OCT-2001 (first entry)
XX
XX Amino acid sequence of a human CLF-1 protein.
DE
XX

KW NNT-1; CLE-1; SCNTFRalpha; nervous system; neuron; nervous system;
KW neuro-muscular function; tumour; immune system; haematopoietic system;
KW reproductive system; liver; skeletal muscle; neurodegenerative disease;
KW amvetrohic lateral sclerosis; Parkinson's disease; Huntington's disease;

KW myofibroblastic mesenchymal tumor; leiomyosarcoma
KW muscular mass; paralysis; cancer; obesity; fertility; endometriosis;
KW blasocyst implantation; thrombosis; retinal disease;
KW retinal pigmentosis.

OS Homo sapiens.
 XX WO200155172-A2.
 XX
 XX 02-AUG-2001.
 PD
 XX 26-JAN-2001; 2001WO-FR000253.
 XX
 XX 27-JAN-2000; 2000FR-00001035.
 PR 12-OCT-2000; 2000FR-00013089.
 XX
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PI Elson G, Gauchat J, Plun-Favreau H, Chevalier S, Gaecan H;
 XX WPI; 2001-488773/53.
 DR N-PSDB; AAH74486.
 XX
 PT A complex comprising a NNT-1 protein and a CLF-1 and/or SCNTFRalpha
 PT protein useful to treat neurodegenerative disease including Parkinson's
 PT and Huntington's, obesity and cancer.
 XX
 XX Claim 2; Page 63-64; 67pp; French.
 XX
 CC The present sequence represents a human CLF-1 protein. The specification
 CC describes a complex comprising a NNT-1 protein and a CLF-1 and/or
 CC SCNTFRalpha protein. The NNT-1/CLF-1 complex is used to modulate activity
 CC of the SCNTFRalpha/gp130/LIFbeta receptor complex, or to induce
 CC phosphorylation of the tyrosine of gp130 and LIFbeta, particularly where
 CC cells expressing the receptor complex are in the central or peripheral
 CC nervous system, in neurons implicated in neuro-muscular function or in
 CC skeletal muscle. The complex or antibodies are also used to decrease the
 CC survival, growth or proliferation of tumour cells or to facilitate the
 CC proliferation and/or inhibit differentiation of cells stocks. The complex
 CC is also used to modulate activity of the gp130/LIFbeta receptor or cells
 CC expressing that receptor, particularly those cells implicated in the
 CC immune, haematopoietic, nervous or reproductive system, the liver or
 CC skeletal muscle. Molecules of the invention may be used to prevent or
 CC treat neurodegenerative diseases including amyotrophic lateral sclerosis,
 CC Parkinson's and Huntington's disease, to repair or regenerate nervous or
 CC muscular tissue or to maintain muscular mass in paralysis patients. They
 CC may also be used to treat cancer, obesity and associated diseases, and to
 CC improve fertility, particularly to avoid endometriosis and/or assist
 CC blastocyst implantation, thrombosis, or retinal disease, particula
 CC retinal pigmentosis
 CC
 CC Sequence 422 AA;
 XX
 SQ
 Query Match 99.5%; Score 2279.5; DB 4; Length 422;
 Best Local Similarity 99.8%; Pred. No. 3,4e-184;
 Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MPAGRRGPAQASARRPPLLP-LLLLCVLAGPRAGSAGHTAVISPODPTLLIGSSLLATC 59
 DB 1 MPAGRRGPAQASARRPPLLP-LLLLCVLAGPRAGSAGHTAVISPODPTLLIGSSLLATC 60
 QY 60 SVHGDPGATAEGLVYTLNRRLLPEISRYVNSTALALANLNGSRGSDMLVCHARD 119
 DB 61 SVHGDPGATAEGLVYTLNRRLLPEISRYVNSTALALANLNGSRGSDMLVCHARD 120
 QY 120 GSILASCLVYGLPPEKPVNISCMKMKDLCTKMPGAGERTLHNNYSLKTKLRMYGQ 179
 DB 121 GSILASCLVYGLPPEKPVNISCMKMKDLCTKMPGAGERTLHNNYSLKTKLRMYGQ 180
 QY 180 DNTCEHYTVGPHSCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDIVVTTDPPD 239
 DB 181 DNTCEHYTVGPHSCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDIVVTTDPPD 240
 QY 240 VHSRVGGLLEDQLSVSWVSPALKDLFLQAKYQIRYRVSDVMKVVDVDSVNOTSCLAG 299
 DB 241 VHSRVGGLLEDQLSVSWVSPALKDLFLQAKYQIRYRVSDVMKVVDVDSVNOTSCLAG 300

QY 300 LKPGTVYFVQRCNPFGIYSGKKAGIWSHSPFAASTPSPSRPDCGACEPGCEPSS 359
 DB 301 LKPGTVYFVQRCNPFGIYSGKKAGIWSHSPFAASTPSPSRPDCGACEPGCEPSS 360
 QY 360 GPVARELKQFLGWLKKAAYCSNLSFRLYDQWRAMQSKHKTRNDEGILPSGRGTARGP 419
 DB 361 GPVARELKQFLGWLKKAAYCSNLSFRLYDQWRAMQSKHKTRNDEGILPSGRGTARGP 420
 QY 420 AR 421
 DB 421 AR 422
 RESULT 9
 ABUS5925
 ID ABUS5925 standard; protein; 422 AA.
 XX
 AC ABUS5925;
 XX
 DT 26-MAR-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO327.
 XX
 XX Human; PRO; secreted protein; transmembrane protein; anti-HIV;
 KW cytosolic; antiarteriosclerotic; antiinflammatory; antidiabetic;
 KW cardiatic; AIDS; acquired immunodeficiency syndrome; cancer;
 KW atherosclerosis; inflammatory disease; diabetic complication;
 KW cardiac injury; organ failure.
 XX
 OS Homo sapiens.
 XX
 XX US2002142959-A1.
 PN
 PD 03-OCT-2002.
 XX
 XX 31-AUG-2001; 2001US-00944654.
 PF
 XX 16-SEP-1998; 98WO-US019330.
 PR 01-DEC-1998; 98WO-US025108.
 PR 22-JUN-1999; 99WO-US012252.
 PR 15-SEP-1999; 99WO-US021090.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 16-DEC-1999; 99WO-US030095.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 25-MAY-2001; 2001US-00866028.
 XX
 XX (GETH) GENENTECH INC.
 PA Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
 PI Gertlisen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
 PI Hillan KJ, Kijavlin IV, Napier MA, Roy MA, Tumas D, Wood WI;
 XX WPI; 2003-174141/17.
 DR N-PSDB; ABX75462.
 XX
 PT New isolated PRO polypeptide and encoding nucleic acid, useful for the
 PT diagnosis and treatment of disorders associated with the PRO polypeptide,
 PT such as AIDS, cancer, atherosclerosis, inflammatory disease and diabetes.
 XX
 PS Claim 12; Fig 14; 17pp; English.
 XX
 CC The invention relates to an isolated PRO polypeptide (a secreted or
 CC transmembrane protein) comprising: (a) at least 80% sequence identity or
 CC positives when compared to any of 15 sequences, fully defined in the

CC specification, lacking or with its associated signal peptide; or (b) at
CC least 80% sequence identity to a sequence encoded by the full-length
CC coding sequence of a DNA deposited in the American Type Culture
CC Collection (ATCC). Also included are: (1) an isolated nucleic acid
CC comprising: (a) at least 80% sequence identity to a nucleotide sequence
CC that encodes a PRO protein; (b) at least 80% sequence identity to a
CC nucleotide sequence or full-length coding sequence with any of 15 fully
CC defined sequences of 957-3441 base pairs given in the specification; or
CC (c) at least 80% sequence identity to a full-length coding sequence of a
CC DNA deposited under ATCC Accession No. 209556, 209508, 209544, 209528,
CC 209530, 209523, 209492, 209532, 209531, 209529, 209527, 209570, 209618,
CC 209621 or 209619; (2) a vector comprising the nucleic acid; (3) a host
CC cell expressing the vector which, when cultured under conditions suitable
CC for expression of the PRO polypeptide, produces the PRO protein; (4) a
CC chimeric molecule comprising PRO fused to a heterologous amino acid
CC sequence; and (5) an anti-PRO antibody. The methods and compositions of
CC the present invention are useful for the diagnosis and treatment of
CC disorders associated with the PRO polypeptide, such as AIDS (acquired
CC immunodeficiency syndrome), cancer, atherosclerosis, inflammatory
CC disease, diabetic complications, cardiac injury and organ failure. The
CC antibodies can also be used in the different screening, therapeutic and
CC biological assays. The present sequence represents a PRO protein

XX Sequence 422 AA;

Query Match	99.5%	Score 2279.5	DB 6	Length 422
Best Local Similarity	99.8%	Pred. No. 3.4e-184		
Best Local 421; Conservative	0	Mismatches 0	Indels 1	Gaps 1

Qy	1	MPGRGRGPAAQASRRRPPPLLP--LLLLCTTGARRAGSAAHTAVISPODPSTLLIGSSLATC	59
Db	1	MPGRRRPAAQASRRPPPLPLPLLLLCVIGARRAGSAAHTAVISPODPSTLLIGSSLATC	60
Qy	60	SVAGDPPGATAEGLYTTINGRLRPELSKVLNASTLATALANINSGRSQSDNIVCHARD	119
Db	61	SVHGDPPGATAEGLYTTINGRLRPELSKVLNASTLATALANINSGRSQSDNIVCHARD	120
Qy	120	GSIIAGSCLVYGLPPEKPVNISGWSKNMKDLTCRWTPGAGHGETFLHTNYSLKTYLRMYGQ	179
Db	121	GSIIAGSCLVYGLPPEKPVNISGWSKNMKDLTCRWTPGAGHGETFLHTNYSLKTYLRMYGQ	180
Qy	180	DNICEEYHTATGSPHSCHPKDIALFTPEYELTWEATRIASASDVYTLTLLDVYTTDPPD	239
Db	181	DNICEEYHTATGSPHSCHPKDIALFTPEYELTWEATRIASASDVYTLTLLDVYTTDPPD	240
Qy	240	VHVSRRVGLEDDQLSVWVSPPALKDFLFOAKYQIRRYVEDSVMKFVVDVSNQTSCLAG	299
Db	241	VHVSRRVGLEDDQLSVWVSPPALKDFLFOAKYQIRRYVEDSVMKFVVDVSNQTSCLAG	300
Qy	300	LKPGTYVFNVORCNPGIYGSKKAGIWSMSHPSTAASPRSRPDPGGGAEPGGGRPS	355
Db	301	LKPGTYVFNVORCNPGIYGSKKAGIWSMSHPSTAASPRSRPDPGGGAEPGGGRPS	360
Qy	360	GPVARELKQFLGWLKTHAYCSNLSFELYDQWAMAMQSHKTRNDEGILLPGGRGTARGP	419
Db	361	GPVARELKQFLGWLKTHAYCSNLSFELYDQWAMAMQSHKTRNDEGILLPGGRGTARGP	420
Qy	420	AR 421	
Db	421	AR 422	

RESULT 10
ABU60235
ID ABU60235 standard; protein; 422 AA.

KW inflammatory disease; atherosclerosis; cardiac injury; AIDS; infertility
KW birth defect; premature aging; diabetes; dog; cat; horse;
KW acquired immunodeficiency syndrome; cow; sheep; pig; goat; rabbit;
KW industry; cytostatic; antiinflammatory; cardiac; antifertility;
KW anti-HIV; antiarteriosclerotic; antidiabetic.

OS Homo sapiens.

PN US2002132768-A1.

PD 19-SEP-2002.

PF 31-AUG-2001; 2001US-00945015.

PR	13-DEC-1997	97US-0067411P
PR	11-DEC-1997	97US-0069334P
PR	11-DEC-1997	97US-0069333AP
PR	11-DEC-1997	97US-0069333S
PR	12-DEC-1997	97US-00694825P
PR	16-DEC-1997	97US-0069619P
PR	16-DEC-1997	97US-0069656P
PR	16-DEC-1997	97US-0069702P
PR	17-DEC-1997	97US-0069873P
PR	17-DEC-1997	97US-0069874P
PR	18-DEC-1997	97US-0068017P
PR	09-FEB-1998	97US-0070440P
PR	09-FEB-1998	97US-0070408P
PR	09-FEB-1998	97US-0070409P
PR	25-FEB-1998	97US-0075545P
PR	16-SEP-1998	98US-00501930
PR	01-DEC-1998	98US-00502510P
PR	16-DEC-1998	98US-00162621
PR	16-DEC-1998	98US-00182501P
PR	22-DEC-1998	98US-0021835P
PR	03-MAR-1999	98US-0013396P
PR	28-JUL-1999	98US-00254311
PR	28-JUL-1999	99US-00501252
PR	15-SEP-1999	99US-00146222P
PR	15-SEP-1999	99US-00201090
PR	30-NOV-1999	99US-00502813
PR	30-NOV-1999	99US-00502840P
PR	01-DEC-1999	99US-00028301
PR	16-DEC-1999	99US-00303095
PR	11-FEB-2000	2000US-00500365
PR	22-FEB-2000	2000US-005004414
PR	02-MAR-2000	2000US-005005431
PR	28-MAY-2000	2000US-005008439
PR	28-JUL-2000	2000US-005014042
PR	01-DEC-2000	2000US-005020710
PR	28-FEB-2001	2001US-005006520
PR	25-MAY-2001	2001US-00066028

PA (GETH) GENENTECH INC.

PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;

PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL
PI Hillan KJ, Kijavini IJ, Napier MA, Roy MA, Tumas D, Wood WI;

DR WPI; 2003-174088/17.

DR N-PSDB; ABX89453.

PT New secreted and transmembrane polypeptides (e.g. PR241, for use in pharmaceuticals, diagnostics or bioreactors), particularly for detecting or treating e.g. cancers, infertility or acquired immunodeficiency syndrome in mammals.

PS Claim 1; Fig 14; 173pp; English.

The invention relates to a human secreted and transmembrane polypeptide (PRO) and the polynucleotide encoding it. The PRO polypeptide or polynucleotide is useful in pharmaceuticals, diagnostics, biosensors or bioeffectors. These are particularly useful for detecting or treating

CC cancers, inflammatory diseases, atherosclerosis, cardiac injury,
 CC infertility, birth defects, premature aging, acquired immunodeficiency
 CC syndrome (AIDS) and diabetic complications in mammals, e.g. humans, dogs,
 CC cats, cattle, horses, sheep, pigs, goats or rabbits. The sequences are
 CC also useful in biotechnological and medical research and in various
 CC industrial applications. Sequences AB060230-AB060245 represent human PRO
 CC polypeptides of the invention
 XX

Sequence 422 AA;

Query Match 99.5%; Score 2279.5; DB 6; Length 422;
 Best Local Similarity 99.8%; Pred. No. 3.4e-184;
 Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MPAGRRGPAQAASARRPPLLP-LLLLCVLAGPARGSGAHTAVISPQDPTLLIGSSLIATC 59
 DB 1 MPAGRRGPAQAASARRPPLLP-LLLLCVLAGPARGSGAHTAVISPQDPTLLIGSSLIATC 60
 QY 60 SVHGDPPGATAGLWTLNRRLLPPELSRVNASTLALANLNGSRQSGDNLYCHARD 119
 DB 61 SVHGDPPGATAGLWTLNRRLLPPELSRVNASTLALANLNGSRQSGDNLYCHARD 120
 QY 120 GSILAGSCLVYGLPPEKPVNISCSKMKDLCRTWPGAGETFLHTNYSIKYLRWYQ 179
 DB 121 GSILAGSCLVYGLPPEKPVNISCSKMKDLCRTWPGAGETFLHTNYSIKYLRWYQ 180
 QY 180 DNTCEHYHTVGPSPCHPKDLALFTPEIWEATNRLGARSVDLTLDIDVTTDPPD 239
 DB 181 DNTCEHYHTVGPSPCHPKDLALFTPEIWEATNRLGARSVDLTLDIDVTTDPPD 240
 QY 240 VHSRVGLEDQSLSVRWSPALADFLFOAKYQIRRYVEDSDVMKVVDDVSNQTSCLAG 299
 DB 241 VHSRVGLEDQSLSVRWSPALADFLFOAKYQIRRYVEDSDVMKVVDDVSNQTSCLAG 300
 QY 300 LKDETVYFVQVRCNPFGIYSKKAGIWESESHPTASTPRSERDPGAGACEPRGSPSS 359
 DB 301 LKDETVYFVQVRCNPFGIYSKKAGIWESESHPTASTPRSERDPGAGACEPRGSPSS 360
 QY 360 GPHARELKOPFLGMLKKAAYGNSLFRLYDQWRAMQSHKTRNDEGLIPSGRGRTARGP 419
 DB 361 GPHARELKOPFLGMLKKAAYGNSLFRLYDQWRAMQSHKTRNDEGLIPSGRGRTARGP 420
 QY 420 AR 421
 DB 421 AR 422

RESULT 11
 ABG72776
 ID ABG72776 standard; protein; 422 AA.

XX 20-FEB-2003. (first entry)
 XX Human cytokine receptor-like factor 1 (CLF-1 or CLR-1) protein.

XX Human, gene expression; bone formation; cartilage formation;
 XX embryonic development; cytokine receptor-like factor 1; CLF-1; CLR-1;
 XX mesenchymal cell differentiation; matrix metalloproteinase 23; MMP23;
 XX bone development; antagonist; agonist; cadherin; CD68; cytokine;
 XX diagnosis; osteodysplasia; osteohypertrophy; osteoblastoma;
 XX osteopetrosis; osteogenesis imperfecta; osteoporosis; osteopenia;
 XX osteoma; osteoblastoma; periodontal disease; hyperparathyroidism;
 XX hypercalcaemia of malignancy; Paget's disease; osteolytic lesion;
 XX bone metastasis; bone loss; immobilization; sex hormone deficiency;
 XX inflammatory disease; rheumatoid arthritis; osteoarthritis;
 XX bone fracture.

XX Homo sapiens.
 XX OS
 XX PN W0200285285-A2.

PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002WO-US012149.
 XX
 PR 18-APR-2001; 2001US-0284786P.
 XX
 PA (AMHP) WYETH.
 XX
 PI Clancy B, Pittman DM;
 DR WPI; 2003-103384/09.
 DR N-PSDB; ABX14013.
 XX
 PT Determining the difference between levels of expression of a number of
 PT genes, useful for diagnosing and treating disorders associated with bone
 PT or cartilage formation or resorption such as osteoporosis and bone
 PT fractures.

XX Disclosure; Page 192-193; 197pp; English.

CC The invention discloses a method for determining the difference between
 CC the levels of expression of a number of, at least 500 genes, during bone
 CC or cartilage formation. The method comprises determining levels of RNA
 CC from the genes to obtain levels of expression and comparing these to a
 CC set of reference levels for each of the genes. Bone formation is an
 CC essential process in embryonic development and plays a critical role in
 CC many diseases and conditions in humans. Two genes found to be regulated
 CC during bone and cartilage formation are the cytokine receptor-like factor
 CC 1 (CLF-1 or CLR-1), which is specifically regulated during mesenchymal
 CC cell differentiation, and matrix metalloproteinase 23 (MMP23), which is
 CC specifically regulated during bone development. Also disclosed is a
 CC computer program for analysing levels of expression of a number of genes,
 CC comprising a number of antagonists or agonists of the genes,
 CC and methods for determining whether a subject has, or is likely to
 CC develop, a disease related to bone or cartilage resorption or formation,
 CC for determining the effectiveness of a treatment intended to stimulate
 CC bone or cartilage formation or resorption, for identifying a compound for
 CC treating, modulating or stimulating a disease related to bone or
 CC cartilage formation possibly acting as a cadherin or CD68 agonist or a
 CC cytokine antagonist. The methods and compositions are useful for
 CC diagnosing and treating disorders associated with bone or cartilage
 CC formation or resorption such as osteodysplasia, osteohypertrophy,
 CC osteoblastoma, osteopetrosis, osteogenesis imperfecta, osteoporosis,
 CC osteopenia, osteoma and osteoblastoma, periodontal disease,
 CC hyperparathyroidism, hypercalcaemia of malignancy, Paget's disease,
 CC osteolytic lesions produced by bone metastasis, bone loss due to
 CC immobilisation or sex hormone deficiency, bone and cartilage loss caused
 CC by an inflammatory disease, rheumatoid arthritis, osteoarthritis and bone
 CC fractures. The sequence presented is the human CLF-1 protein

XX Sequence 422 AA;

Query Match 99.5%; Score 2279.5; DB 6; Length 422;
 Best Local Similarity 99.8%; Pred. No. 3.4e-184;
 Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MPAGRRGPAQAASARRPPLLP-LLLLCVLAGPARGSGAHTAVISPQDPTLLIGSSLIATC 59
 DB 1 MPAGRRGPAQAASARRPPLLP-LLLLCVLAGPARGSGAHTAVISPQDPTLLIGSSLIATC 60
 QY 60 SVHGDPPGATAGLWTLNRRLLPPELSRVNASTLALANLNGSRQSGDNLYCHARD 119
 DB 61 SVHGDPPGATAGLWTLNRRLLPPELSRVNASTLALANLNGSRQSGDNLYCHARD 120
 QY 120 GSILAGSCLVYGLPPEKPVNISCSKMKDLCRTWPGAGETFLHTNYSIKYLRWYQ 179
 DB 121 GSILAGSCLVYGLPPEKPVNISCSKMKDLCRTWPGAGETFLHTNYSIKYLRWYQ 180
 QY 180 DNTCEHYHTVGPSPCHPKDLALFTPEIWEATNRLGARSVDLTLDIDVTTDPPD 239
 DB 181 DNTCEHYHTVGPSPCHPKDLALFTPEIWEATNRLGARSVDLTLDIDVTTDPPD 240
 QY 240 VHSRVGLEDQSLSVRWSPALADFLFOAKYQIRRYVEDSDVMKVVDDVSNQTSCLAG 299

DB 241 VHSRVGGLLEDQLSVWVSPALPKDFLFOAKYQIRRVSDVMKVVDVSNQTSCLRLAG 300
QY 300 LKRGTYFVQVRCNPFPGIGSKKAGIWSWSHPTAASPTSPSRPPGGGACBPRGGEPPSS 359
DB 301 LKRGTYFVQVRCNPFPGIGSKKAGIWSWSHPTAASPTSPSRPPGGGACBPRGGEPPSS 360
QY 360 GPVRRRLKQFLGWLKKGAVCSNLSFRLYDQWRAMQKSHKTRNODGILPSGRGTARGP 419
DB 361 GPVRRRLKQFLGWLKKGAVCSNLSFRLYDQWRAMQKSHKTRNODGILPSGRGTARGP 420
QY 420 AR 421
DB 421 AR 422

RESULT 12
ABU64921
ID ABU64921 standard; protein; 422 AA.
XX
AC ABU64921;
XX
DT 15-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO327.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW Cornelia de Lange syndrome; gene therapy; immune disorder;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defect; premature aging; cardiac injury; AIDS; cancer;
KW diabetic complication.
XX
OS Homo sapiens.
XX
PN US2002173463-A1.
XX
PD 21-NOV-2002.
XX
PF 31-AUG-2001; 2001US-00944944.
XX
PR 03-DEC-1997; 97US-0067411P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 12-DEC-1997; 97US-0069425P.
PR 16-DEC-1997; 97US-0069694P.
PR 16-DEC-1997; 97US-0069702P.
PR 17-DEC-1997; 97US-0069870P.
PR 17-DEC-1997; 97US-0069873P.
PR 18-DEC-1997; 97US-0068017P.
PR 05-JAN-1998; 98US-0070440P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-FEB-1998; 98US-0075945P.
PR 16-MAR-1998; 98MO-US019330.
PR 01-DEC-1998; 98MO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 22-DEC-1998; 98US-0113296P.
PR 02-JUN-1999; 99MO-US012252.
PR 28-JUL-1999; 99US-0146222P.
PR 15-SEP-1999; 99MO-US021090.
PR 30-NOV-1999; 99MO-US028313.
PR 30-NOV-1999; 99MO-US028409.
PR 01-DEC-1999; 99MO-US028301.
PR 16-DEC-1999; 99MO-US030095.
PR 11-FEB-2000; 2000MO-US003565.
PR 22-FEB-2000; 2000MO-US004414.
PR 02-MAR-2000; 2000MO-US005841.
PR 30-MAR-2000; 2000MO-US008439.
PR 22-MAY-2000; 2000MO-US014042.
PR 28-JUL-2000; 2000MO-US020710.
PR 01-DEC-2000; 2000MO-US032678.

PR 28-FEB-2001; 2001MO-US006520.
PR 25-MAY-2001; 2001US-00866028.
XX
PA (GENTH) GENENTECH INC.
XX
PI Baker KP, Bostein D, Bacon DL, Ferrara N, Filvaroff E;
PI Gertsen ME, Goddard A, Godowski PJ, Grimaldi JC, Guney AL;
PI Hillan KJ, Kijavlin IU, Napier MA, Roy MA, Tumas D, Wood WI;
DR WPI; 2003-311003/30.
DR N-PSDB; ABX96790.
XX
PT New transmembrane polypeptides and polynucleotides useful for chromosome
PT identification, tissue typing, gene therapy, in chromosome and gene
PT mapping, or as molecular weight markers.
XX
XX
XX Claim 12; Fig 14; 172pp; English.
XX
XX
CC The invention relates to an isolated nucleic acid encoding a secreted/
CC transmembrane polypeptide (designated as PRO proteins). 15 PRO
CC polypeptides and their encoding polynucleotides are disclosed. Also
CC included are a vector comprising the PRO nucleic acid, a host cell
CC comprising the vector, a process for producing a PRO polypeptide (by
CC culturing the host cell under conditions for the expression of the PRO
CC polypeptide, and recovering the PRO polypeptide from the cell culture, an
CC isolated polypeptide having at least 80% amino acid sequence identity to
CC the PRO polypeptides), a chimeric molecule comprising PRO fused to a
CC heterologous amino acid sequence and an antibody which specifically binds
CC to PRO. The PRO nucleotide sequences are useful as hybridisation probes,
CC in chromosome and gene mapping, in generating sense and antisense RNA or
CC DNA, in generating transgenic or knock-out animals which can be used in
CC the development and screening of therapeutically useful reagents, and in
CC gene therapy. The polypeptides may be used as molecular weight markers
CC for protein electrophoresis purposes. The PRO polypeptides and nucleic
CC acids may also be used for chromosome identification, and tissue typing.
CC PRO241 (identified as Chordin) is a candidate gene for Cornelia de Lange
CC syndrome. Other PRO proteins are variously implicated in immune
CC disorders, inflammatory disease, organ failure, atherosclerosis, cardiac
CC injury, infertility, birth defects, premature aging, cardiac injury,
CC AIDS, cancer and diabetic complications. The present sequence represents
CC a PRO protein
XX
SQ Sequence 422 AA;
XX
Query Match 99.5%; Score 2279.5; DB 6; Length 422;
Best Local Similarity 99.8%; Pred. No. 3,4e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MPAGRRGPAQASARRPPLLP-LILLICVGPARGAGARTAVISPODPTLIGSSILATC 59
DB 1 MPAGRRGPAQASARRPPLLP-LILLICVGPARGAGARTAVISPODPTLIGSSILATC 60
QY 60 SVHGDPPGATAGLTYTLNGRRLLPELISRVLNASTLALALAMINGSRSGDNLVCHARD 119
DB 61 SVHGDPPGATAGLTYTLNGRRLLPELISRVLNASTLALALAMINGSRSGDNLVCHARD 120
QY 120 GSTLAGSCLYVGLPEPKPVNISCWKNMDLTCRWTPGAGHGFLLHTNYSLKTKLAWYQ 179
DB 121 GSTLAGSCLYVGLPEPKPVNISCWKNMDLTCRWTPGAGHGFLLHTNYSLKTKLAWYQ 180
QY 180 DNTCEEHYTVGPHSCHIPKDLALFTPEYETWEATNRIGSARSBDVLTLIDVYTTDPPD 239
DB 181 DNTCEEHYTVGPHSCHIPKDLALFTPEYETWEATNRIGSARSBDVLTLIDVYTTDPPD 240
QY 240 VHSRVGGLLEDQLSVWVSPALPKDFLFOAKYQIRRVSDVMKVVDVSNQTSCLRLAG 299
DB 241 VHSRVGGLLEDQLSVWVSPALPKDFLFOAKYQIRRVSDVMKVVDVSNQTSCLRLAG 300
QY 300 LKRGTYFVQVRCNPFPGIGSKKAGIWSWSHPTAASPTSPSRPPGGGACBPRGGEPPSS 359
DB 301 LKRGTYFVQVRCNPFPGIGSKKAGIWSWSHPTAASPTSPSRPPGGGACBPRGGEPPSS 360
QY 360 GPVRRRLKQFLGWLKKGAVCSNLSFRLYDQWRAMQKSHKTRNODGILPSGRGTARGP 419

Db 361 GPYRREIKQFLGWLKKGAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRGTARGP 420
QY 420 AR 421
Db 421 AR 422

RESULT 13
ABUS8355
ID ABUS8355 standard; protein; 422 AA.
XX
AC ABUS8355;
XX
DT 14-APR-2003 (first entry)
XX
DE Novel human secreted protein PRO327.

XX Human; antiinflammatory; antiarteriosclerotic; cardiac; gynecological;
KM anti-HIV; cytostatic; antidiabetic; BMP-agonist; BMP-Antagonist;
KM cytokine-agonist; cytokine-antagonist; gene-Therapy;
KM inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KM infertility; birth defect; premature aging; AIDS; cancer;
KM diabetic complication.

XX Homo sapiens.

XX US2002150976-A1.

XX 17-OCT-2002.

XX 30-AUG-2001; 2001US-00943851.

XX 03-DEC-1997; 97US-0067411P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 16-DEC-1997; 97US-0069684P.
PR 16-DEC-1997; 97US-0069686P.
PR 16-DEC-1997; 97US-0069702P.
PR 17-DEC-1997; 97US-0069870P.
PR 17-DEC-1997; 97US-0068017P.
PR 18-DEC-1997; 97US-0068017P.
PR 05-JAN-1998; 98US-0070440P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 16-SEP-1998; 98US-0075945P.
PR 16-SEP-1998; 98US-0075945P.
PR 01-DEC-1998; 98US-0075945P.
PR 16-DEC-1998; 98US-0075945P.
PR 16-DEC-1998; 98US-0075945P.
PR 22-DEC-1998; 98US-0075945P.
PR 22-DEC-1998; 98US-0075945P.
PR 03-MAR-1999; 99US-00254311.
PR 02-JUN-1999; 99US-00254311.
PR 28-JUL-1999; 99US-0146222P.
PR 15-SEP-1999; 99US-0146222P.
PR 30-NOV-1999; 99US-0146222P.
PR 30-NOV-1999; 99US-0146222P.
PR 01-DEC-1999; 99US-0146222P.
PR 16-DEC-1999; 99US-0146222P.
PR 11-FEB-2000; 2000US-0003565.
PR 22-FEB-2000; 2000US-0003565.
PR 02-MAR-2000; 2000US-0003565.
PR 30-MAR-2000; 2000US-0003565.
PR 22-MAY-2000; 2000US-0003565.
PR 28-JUL-2000; 2000US-0003565.
PR 01-DEC-2000; 2000US-0003565.
PR 28-FEB-2001; 2001US-0003565.
PR 25-MAY-2001; 2001US-0003565.

XX (GETH) GENENTECH INC.

XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
PI Hillan KU, Kijavini IO, Napier MA, Roy MA, Tumas D, Wood WT;
XX WPI; 2003-198285/19.
DR N-PSDB; ABX78444.

XX New isolated PRO polypeptide and encoding nucleic acids, useful for the
PT diagnosis and treatment of disorders such as inflammatory disease,
PT atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic
PT complications.

XX Claim 12; Fig 14; 17pp; English.

XX The invention describes a novel isolated PRO polypeptide. The methods and
CC compositions of the present invention are useful for the diagnosis and
CC treatment of disorders such as inflammatory disease, organ failure,
CC atherosclerosis, cardiac injury, infertility, birth defects, premature
CC aging, AIDS, cancer, diabetic complications and mutations in general.
XX This is the amino acid sequence of a novel human secreted PRO protein

XX Sequence 422 AA;

Query Match 99.5%; Score 2279.5; DB 6; Length 422;
Best Local Similarity 99.8%; Pred. No. 3,4e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLAGAPAGAGATAVISPODPTLLIGSSLLATC 59
Db 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLAGAPAGAGATAVISPODPTLLIGSSLLATC 60
QY 60 SVHGDPGATAEGLVYTLNKRRLPPELSRYLNASTLALANLNGSRQSGDNVYCHARD 119
Db 61 SVHGDPGATAEGLVYTLNKRRLPPELSRYLNASTLALANLNGSRQSGDNVYCHARD 120
QY 120 GSILAGSCLVYGLPPEKPVNISCSKXMDLTCRWMPGAGETFLHTNYSLKYLRYGQ 179
Db 121 GSILAGSCLVYGLPPEKPVNISCSKXMDLTCRWMPGAGETFLHTNYSLKYLRYGQ 180
QY 180 DNTCEHYHTVSPHSCHIPKDALFTPEYIWEATNRLGARSQVLTLDLIDVYTTDPPD 239
Db 181 DNTCEHYHTVSPHSCHIPKDALFTPEYIWEATNRLGARSQVLTLDLIDVYTTDPPD 240
QY 240 VHSRVGLEDQSVWVSPALPDKLFOAKYIIRRVESDVWKYVDVSNQTSCLAG 299
Db 241 VHSRVGLEDQSVWVSPALPDKLFOAKYIIRRVESDVWKYVDVSNQTSCLAG 300
QY 300 LKPGTYVYVQVRCNPGIYSGKAGIWSKSHPTASTPSSRPGGGACBPBGSS 359
Db 301 LKPGTYVYVQVRCNPGIYSGKAGIWSKSHPTASTPSSRPGGGACBPBGSS 360
QY 360 GPYRREIKQFLGWLKKGAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRGTARGP 419
Db 361 GPYRREIKQFLGWLKKGAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRGTARGP 420
QY 420 AR 421
Db 421 AR 422

RESULT 14

ABUS7241
ID ABUS7241 standard; protein; 422 AA.

XX ABUS7241;
XX

XX 04-APR-2003 (first entry)
XX

XX Human PRO327 protein.
XX

XX Human; antiinflammatory; antiarteriosclerotic; cardiac;
KM anti-infertility; anti-HIV; cytostatic; antidiabetic; transmembrane;

KW anti-inflammatory; anti-HIV; antiarteriosclerotic; cardiant; infertility;
KW anti-infertility; cytosratic; antidiabetic; gene therapy; birth defect;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW premature aging; AIDS; cancer; diabetic complication.
XX
XX Homo sapiens.
XX OS
XX PN US2002142958-A1.
XX
XX 03-OCT-2002.
XX PD
XX PF 30-AUG-2001; 2001US-00943762.
XX
XX 16-SEP-1998; 98WO-US019330.
PR 01-DEC-1998; 98WO-US025108.
PR 22-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 25-MAY-2001; 2001US-00866028.
XX
XX (GENTH) GENENTECH INC.
XX PA
PI Baker KP, Botstein D, Baton DL, Ferrara N, Filvaroff E;
PI Gerltsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
XX
XX WPI; 2003-174140/17.
DR N-PSDB; ABX71077.
XX
XX New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
XX Claim 1; Fig 14; 173pp; English.
XX PS
XX This invention relates to a nucleotide sequence encoding an isolated
CC secreted and/or transmembrane protein. The nucleotide sequences of the
CC invention may have anti-inflammatory, antiarteriosclerotic, cardiant, anti-
CC -infertility, anti-HIV, cytosratic and antidiabetic activities and may be
CC used in gene therapy. The nucleic acids and polypeptides are useful for
CC treating inflammatory diseases, organ failure, atherosclerosis, cardiac
CC injury, infertility, birth defects, premature aging, AIDS, cancer, or
CC diabetic complications. The nucleic acids are useful as hybridisation
CC probes, in chromosome and gene mapping, and in generating antisense RNA
CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
CC biosensors or bioreactors. Both are useful in tissue typing. The present
CC sequence represents a protein encoded by the nucleic acids of the
XX invention
XX
SQ Sequence 422 AA;
Query Match 99.5%; Score 2279.5; DB 6; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.4e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MPAGRRGPAAGSARPPPLP-LILLCYLAGAPRAGSGAHTAVISPDPTLLIGSSLLATC 59
DB 1 MPAGRRGPAAGSARPPPLP-LILLCYLAGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
QY 60 SVHGDPPGATAGELVYTLNGRRLLPELSRVIANASTLALANLNGSRQSRGDNLVGHARD 119
|||||

DB 61 SVHGDPPGATAGELVYTLNGRRLLPELSRVIANASTLALANLNGSRQSRGDNLVGHARD 120
QY 120 GSIIAGSCLYVGLPPEEPVNI SCSSKMKDLTCRWTPGAGETPLHTNYSLKXKLRMYGQ 179
DB 121 GSIIAGSCLYVGLPPEEPVNI SCSSKMKDLTCRWTPGAGETPLHTNYSLKXKLRMYGQ 180
QY 180 DNTCEHYHWGPHSCCHPKDLALFTPYEIWEATNRLGARSVDLTLDIDVYTTDPPD 239
DB 181 DNTCEHYHWGPHSCCHPKDLALFTPYEIWEATNRLGARSVDLTLDIDVYTTDPPD 240
QY 240 VHSRVVGLLEDQLSVRNVSPPALKDPLFOAKYQIRYVEVDSVDMKVVDVSNQTSCLAG 299
DB 241 VHSRVVGLLEDQLSVRNVSPPALKDPLFOAKYQIRYVEVDSVDMKVVDVSNQTSCLAG 300
QY 300 LKPGTVYVQVRCNPFYGSCKAGISSEMSHPPTASTPSEPRGPGGACPEPRGEPSS 359
DB 301 LKPGTVYVQVRCNPFYGSCKAGISSEMSHPPTASTPSEPRGPGGACPEPRGEPSS 360
QY 360 GVPREELKQFLGWLKKAHVCNLSFRLYDQWRAMWQSKHKTNRNDEGILPSGRRTARGP 419
DB 361 GVPREELKQFLGWLKKAHVCNLSFRLYDQWRAMWQSKHKTNRNDEGILPSGRRTARGP 420
QY 420 AR 421
DB 421 AR 422

RESULT 15
ABUS6306
ID ABUS6306 standard; protein; 422 AA.
XX
XX ABUS6306;
AC
XX
DT 31-MAR-2003 (first entry)
XX
XX Human secreted/transmembrane protein, PRO327.
XX
XX Human; PRO; anti-inflammatory; antiarteriosclerotic; cardiant;
KW gynecological; anti-HIV; cytosratic; antidiabetic; inflammatory disease;
KW organ failure; atherosclerosis; cardiac injury; infertility;
KW birth defect; premature aging; AIDS; acquired immunodeficiency syndrome;
KW cancer; diabetic complication.
XX
XX Homo sapiens.
XX OS
XX PN US2002132981-A1.
XX
XX 19-SEP-2002.
XX PF
XX 30-AUG-2001; 2001US-00944396.
XX
XX 03-DEC-1997; 97US-0067411P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 16-DEC-1997; 97US-0069694P.
PR 16-DEC-1997; 97US-0069696P.
PR 16-DEC-1997; 97US-0069702P.
PR 17-DEC-1997; 97US-0069870P.
PR 17-DEC-1997; 97US-0069873P.
PR 18-DEC-1997; 97US-0068017P.
PR 05-JAN-1998; 98US-0070440P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-FEB-1998; 98US-0075945P.
PR 16-SEP-1998; 98WO-US019330.
PR 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 22-DEC-1998; 98US-0113266P.
PR 02-JUN-1999; 99WO-US012252.
PR 28-JUL-1999; 99US-0146222P.
PR 15-SEP-1999; 99WO-US021090.

PR 30-NOV-1999; 99MO-US028313.
PR 30-NOV-1999; 99MO-US028409.
PR 01-DEC-1999; 99MO-US028301.
PR 16-DEC-1999; 99MO-US030095.
PR 11-FEB-2000; 2000MO-US003565.
PR 22-FEB-2000; 2000MO-US004414.
PR 02-MAR-2000; 2000MO-US005841.
PR 30-MAR-2000; 2000MO-US008439.
PR 22-MAY-2000; 2000MO-US014042.
PR 28-JUL-2000; 2000MO-US020710.
PR 01-DEC-2000; 2000MO-US032678.
PR 28-FEB-2001; 2001MO-US006520.
PR 25-MAY-2001; 2001US-00866028.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
PI Geritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
PI Hillan KJ, Kljavin ID, Napier MA, Roy MA, Tumas D, Wood WI;
XX
DR MPI: 2003-14746/14.
DR N-PSDB; ABX75909.
XX
XX
PT New isolated PRO polypeptide and encoding nucleic acids, useful for the
PT diagnosis and treatment of disorders such as inflammatory disease,
PT atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic
PT complications.
XX
PS Claim 12; Fig 14; 171pp; English.
XX
CC The invention relates to an isolated PRO polypeptide having at least 80%
CC amino acid sequence identity to and scoring at least 80% positives when
CC compared to any of 15 fully defined sequences of 235-954 amino acids,
CC given in the specification. Also included are: (1) an isolated PRO
CC nucleic acid having at least 80% nucleic acid sequence identity to a
CC nucleotide sequence that encodes PRO or its extracellular domain, and
CC comprising any of 15 fully defined nucleotide sequences of 957-3441 bp,
CC given in the specification and deposited under ATCC accession number
CC 209526, 209508, 209524, 209528, 209530, 209523, 209492, 209532, 209531,
CC 209529, 209527, 209570, 209618, 209621 and 209619; (2) a vector
CC comprising the PRO nucleic acid; (3) a host cell comprising the vector;
CC (4) producing PRO polypeptides, comprising culturing the cell for
CC expression of the PRO polypeptide and recovering the PRO polypeptide from
CC the cell culture; (5) a chimeric molecule comprising PRO fused to a
CC heterologous amino acid sequence, and (6) an anti-PRO antibody. The
CC methods and compositions are useful for the diagnosis and treatment of
CC disorders such as inflammatory disease, organ failure, atherosclerosis,
CC cardiac injury, infertility, birth defects, premature aging, AIDS
CC (acquired immunodeficiency syndrome), cancer, diabetic complications and
CC mutations in general. The present sequence is a PRO polypeptide
XX
SQ Sequence 422 AA;
Query Match 99.5%; Score 2279.5; DB 6; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.4e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MPAGRRGPAQAASARPPPLLP-LLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSSLATC 59
DB 1 MPAGRRGPAQAASARPPPLLP-LLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSSLATC 60
QY 60 SVHGDPPGATAEGLTYTLNGRRLLPPELSRYLANASTLALANLNGSRKRGDNLVCHARD 119
DB 61 SVHGDPPGATAEGLTYTLNGRRLLPPELSRYLANASTLALANLNGSRKRGDNLVCHARD 120
QY 120 GSIIAGSCLYVGLPPEKPVNISCSKMKMDLTCTWTPGAGGETFLHTNYSLKTKLRWYGG 179
DB 121 GSIIAGSCLYVGLPPEKPVNISCSKMKMDLTCTWTPGAGGETFLHTNYSLKTKLRWYGG 180
QY 180 DNTCEBYHTVGPHSCHIPKDLALFTPEYIWEATNRLGARSADVLTLDIVVTTDPPPD 239
DB 181 DNTCEBYHTVGPHSCHIPKDLALFTPEYIWEATNRLGARSADVLTLDIVVTTDPPPD 240

QY 240 VHSRVVGLLEDQSLVVRWVSPPALKDFLFOAKYQIRYRVEDSDVMKVVDVSNQTSCLAG 299
DB 241 VHSRVVGLLEDQSLVVRWVSPPALKDFLFOAKYQIRYRVEDSDVMKVVDVSNQTSCLAG 300
QY 300 LKPGTYVQVRCNPFGIYGSKKAGIWSWSHPTAASTPSEBPGPGGACBPBGSPSS 359
DB 301 LKPGTYVQVRCNPFGIYGSKKAGIWSWSHPTAASTPSEBPGPGGACBPBGSPSS 360
QY 360 GPVRRRLKQFLGWLKKGAYCSNLSFRLYDQWRAMQKSHKTRNODGILLPSGRGRTARGP 419
DB 361 GPVRRRLKQFLGWLKKGAYCSNLSFRLYDQWRAMQKSHKTRNODGILLPSGRGRTARGP 420
QY 420 AR 421
DB 421 AR 422

Search completed: February 24, 2005, 03:33:08
Job time : 79 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	332	14.5	288	2	B59405	prolactin receptor
2	332	14.5	376	2	A59405	prolactin receptor
3	332	14.5	622	2	A40144	prolactin receptor
4	323	14.1	918	2	A36337	membrane glycoprotein
5	317.5	13.9	917	2	I49659	glycoprotein 130 -
6	316	13.8	830	2	I50455	prolactin receptor
7	314.5	13.7	918	2	A44257	interleukin-6 signal
8	313	13.7	310	2	A29884	prolactin receptor
9	313	13.7	412	2	A41070	prolactin receptor
10	313	13.7	610	2	A34631	prolactin receptor
11	313	13.7	610	2	A36116	lactogen receptor
12	309.5	13.5	292	2	I77552	prolactin receptor
13	309.5	13.5	303	2	I77554	prolactin receptor
14	309.5	13.5	608	2	I53292	prolactin receptor
15	308	13.4	831	2	J01655	prolactin receptor
16	306.5	13.4	581	2	I45971	prolactin receptor
17	300.5	13.1	616	2	A30304	prolactin receptor
18	263.5	11.5	630	2	I51086	prolactin receptor
19	255.5	11.2	837	2	A34898	prolactin receptor
20	249	10.9	372	2	I58141	granulocyte colony
21	242.5	10.6	771	2	B38252	ciliary neurotrophin
22	242.5	10.6	783	2	JH0339	granulocyte colony
23	242.5	10.6	863	2	C38252	granulocyte colony
24	236	10.3	372	1	UHHUCN	ciliary neurotrophin
25	211.5	9.2	362	2	S60614	growth promoting a
26	211.5	9.2	422	2	I37891	interleukin-11 rece
27	208.5	9.1	432	2	I48343	interleukin-11 rece
28	201	8.8	466	1	A11242	interleukin-6 rece
29	200	8.7	1097	1	S17308	leukemia inhibitor

30	199.5	8.7	460	2	JL10145	interleukin-6 receptor
31	199	8.7	156	2	AT38868	prolactin receptor
32	194.5	8.5	805	2	S68441	leptin receptor, s
33	194.5	8.5	892	2	S68439	leptin receptor, s
34	194.5	8.5	894	2	S68437	leptin receptor, s
35	194.5	8.5	900	2	S68440	leptin receptor, s
36	194.5	8.5	1162	2	S68438	leptin receptor, s
37	194	8.5	625	2	S35317	hematopoietic growth factor
38	191.5	8.4	440	2	JL10144	interleukin-6 receptor
39	191	8.3	150	2	B34631	lactogen receptor
40	190.5	8.3	1162	2	PC4184	leptin receptor, O
41	190	8.3	626	2	S37622	proto-oncogene - src
42	187	8.2	1092	2	JYX312	differentiation-stimulating factor
43	186.5	8.1	579	2	B45266	MPL-K protein precursor
44	186.5	8.1	635	2	A45266	MPL-K protein precursor
45	184	8.0	895	2	S74225	leptin receptor, I

ALIGNMENTS

RESULT 1

prolactin receptor short form S1b precursor, breast cancer cells T-47D - human

C|Species: Homo sapiens (man)

C|Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C|Accession: B59405; B49400

R|Hu, Z.Z.; Meng, J.; Dufau, M.L.

J. Biol. Chem. 276, 41086-41094, 2001

A|Title: Isolation and characterization of two novel forms of the human prolactin receptor

A|Reference number: A59405; MUID:21538812; PMID:11518703

A|Accession: B59405

A|Status: preliminary

A|Molecule type: DNA

A|Residues: 1-288 <HU1>

A|Cross-References: UNIPROT:Q96P36; GB:AF214012; PIDN:AF214012.1

R|Hu, Z.Z.

submitted to GenBank, December, 1999

A|Reference number: A49400

A|Accession: B49400

A|Status: preliminary

A|Molecule type: DNA

A|Residues: 1-288 <HU2>

A|Cross-References: GB:AF214012; PIDN:AF214012.1

C|Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor 'la-casain gene promoter activation, w1ch S1b more effective than S1a. However, their li

C|Genetics:

A|Gene: GDB:PRLR

A|Cross-References: GDB:120315; OMIM:176761

A|Map position: 5p13.3-5p13.1

C|Keywords: glycoprotein; transmembrane protein

F|1-24/Domain: signal sequence #status predicted <SIG>

F|25-268/Product: prolactin receptor, short form S1b #status predicted <MAN>

F|35-221/Domain: cytokine receptor homology <CRS>

F|59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.5%; Score 332; DB 2; Length 288;

Best Local Similarity 37.1%; Pred. No. 2.1e-18;

Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

Dy 122 ILAAGCLYVG-LPEKRPVNISCSKXMKDLTCRTPAGHGETPLHTVYSLKYKLRWGQD 180

Dy 15 LPLNTCLLNLQOLPPGKREIFKCRSPNKETPTCWRPPTDGG--LPLVYSILYHREGETLM 72

Dy 181 NTCEEHVTVGPHSCHPKD-LALFTPEYIWEATNRLGSARSVDLTLDIVVTTDPPPD 239

Dy 73 HCEPDYITGSPNSCHGEKQYTSIMRTIYIMVNAITNQSSFSDELIVDVYIYIVQDPPEL 132

Dy 240 VHTSRVGGLEDQSLSEVRV--SPPALXDF--LFCARKQIIRYVEDSYDWKVKVDVSNQTS 294

Dy 133 LNV-EYKQEPDRKPRYIMIKMSPTLLIDLKTKGFTLLYELIKLPEKAAEWI-IHAGQOTE 190

Dy 295 CRLAGLKPGLTVYFVQVRCPNFGIYGSKKAGIWEWSHPTAATP 338

Db 191 FKILSLHPGQKYLIVQRCKP-----DHGYWSAMSPATFIQIP 227

RESULT 2
A59405
prolactin receptor short form S1a precursor, breast cancer cells T-47D - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: A59405; A49400
R:Hu, Z.Z.; Meng, J.; Dufau, M.L.
J. Biol. Chem. 276, 41086-41094, 2001
A:Title: Isolation and characterization of two novel forms of the human prolactin receptor
A:Reference number: A59405; MUID:21538812; PMID:11516703
A:Accession: A59405
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <HU1>
A:Cross-references: UNIPROT:Q96P35; GB:AF214012; PIDN:AF214012.1
R:Hu, Z.Z.
submitted to GenBank, December, 1999
A:Reference number: A49400
A:Accession: A49400
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <HU2>
A:Cross-references: GB:AF214012; PIDN:AF214012.1
C:Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor. The casein gene promoter activation, with S1a less effective than S1b. However, their 11 kDa COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. #expe
C:Genetics:
A:Gene: GDB:PRLR
A:Cross-references: GDB:120315; OMIM:176761
A:Map position: 5p13.3-5p13.1
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-376/Product: prolactin receptor, short form S1a #status predicted <MAT>
F:36-221/Domain: cytokine receptor homology <CRS>
F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.5%; Score 332; DB 2; Length 376;
Best Local Similarity 37.1%; Pred. No. 2.9e-18;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

QY 122 ILAAGSLVYG-LPPEKPVNISCSKMKMDLTCMTPGAHGETFLHTNYSLKTKLRWYGQD 180
Db 15 LFLNTCLANGQLPFGKPELFCRSPKKEFTFCWMPGTDG--LPTNYSLTTHRGSETLM 72
QY 181 NTCEBYHTVGPCHSCHIIPKD-LALFTPYEITWEATNRLGSARSDVLTLDILDVTTDPPDP 239
Db 73 HECPPDYITGGPNSCHFQKQYTSWWRITIMVNATNMGSSFSDELVDVTVYVQDPPPLE 132
QY 240 VAVSRVGLIEDQLSRVW--SPALKDF---LFQAKYQIRYVEDSDVMKVVDDVSNQTS 294
Db 133 LAV-EVKQPEDRKPRPLIMKMSPTLLIDLKTGWFLLYIRLKEKAEME-IHFAQQQTE 190
QY 295 CRLAGLPGTVYFVOVRCNPFYIGSKKAGIWESEHPTAASP 338
Db 191 FKILSLHPGQKYLIVQRCKP-----DHGYWSAMSPATFIQIP 227

RESULT 3
A40144
prolactin receptor long form precursor, hepatoma and breast cancer cells - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: A40144; A57018
R:Boutin, J.M.; Edey, M.; Shirota, M.; Jolicœur, C.; Lesueur, L.; Ali, S.; Gould, D.;
Mol. Endocrinol. 3, 1455-1461, 1989
A:Title: Identification of a cDNA encoding a long form of prolactin receptor in human he
A:Reference number: A40144; MUID:90114212; PMID:2558309
A:Accession: A40144
A:Molecule type: mRNA

A:Residues: 1-622 <BOU>
A:Cross-references: UNIPROT:P16471; GB:M31661; NID:9190361; PIDN:AAA60174.1; PID:9190362
R:Pub. G.; Wells, J.A. 270, 13133-13137, 1995
J. Biol. Chem. 270, 13133-13137, 1995
A:Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell li
A:Reference number: A57018; MUID:95286597; PMID:7766908
A:Accession: A57018
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 25-228, 'AW' <RES>
A:Cross-references: GB:S78505; NID:9999114; PIDN:AA834470.1; PID:9999115
C:Genetics:
A:Gene: GDB:PRLR
A:Cross-references: GDB:120315; OMIM:176761
A:Map position: 5p13.3-5p13.1
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-622/Product: prolactin receptor, long form #status predicted <MAT>
F:36-221/Domain: cytokine receptor homology <CRS>
F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.5%; Score 332; DB 2; Length 622;
Best Local Similarity 37.1%; Pred. No. 5.5e-18;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

QY 122 ILAAGSLVYG-LPPEKPVNISCSKMKMDLTCMTPGAHGETFLHTNYSLKTKLRWYGQD 180
Db 15 LFLNTCLANGQLPFGKPELFCRSPKKEFTFCWMPGTDG--LPTNYSLTTHRGSETLM 72
QY 181 NTCEBYHTVGPCHSCHIIPKD-LALFTPYEITWEATNRLGSARSDVLTLDILDVTTDPPDP 239
Db 73 HECPPDYITGGPNSCHFQKQYTSWWRITIMVNATNMGSSFSDELVDVTVYVQDPPPLE 132
QY 240 VAVSRVGLIEDQLSRVW--SPALKDF---LFQAKYQIRYVEDSDVMKVVDDVSNQTS 294
Db 133 LAV-EVKQPEDRKPRPLIMKMSPTLLIDLKTGWFLLYIRLKEKAEME-IHFAQQQTE 190
QY 295 CRLAGLPGTVYFVOVRCNPFYIGSKKAGIWESEHPTAASP 338
Db 191 FKILSLHPGQKYLIVQRCKP-----DHGYWSAMSPATFIQIP 227

RESULT 4
A36337
membrane glycoprotein gp130 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
C:Accession: A36337
R:Hihi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; MUID:91084844; PMID:2261637
A:Accession: A36337
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <HIB>
A:Cross-references: UNIPROT:P40189; GB:M57230; NID:9186353; PIDN:AAA59155.1; PID:9186354
C:Genetics:
A:Gene: GDB:IL6ST; GP130
A:Cross-references: GDB:126725; OMIM:600694
A:Map position: 5q11-5q11
C:Keywords: glycoprotein; membrane protein
F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 14.1%; Score 323; DB 2; Length 918;
Best Local Similarity 28.2%; Pred. No. 4.5e-17;
Matches 87; Conservative 52; Mismatches 151; Indels 18; Gaps 8;

QY 42 ISPDPPTLLIGSSSLATGCVHG---DPRGATAGLWTLNGRRRLPPELSRVLNASTLAIA 98
Db 31 IIPESVVOQLHSNFTAVCVLKEKCMDFVFNANVYVWKTNHTTPEQYTTINRTASSVT 90
QY 99 LANLNGRSRSGDNIVCHARDSILAGSLVYGLPPEKPVNISCSKMKMDLTCMTPGA 158

Db 91 FTDLASINIGLTCNLTLPFGLEQNVYGITIISGLPPEKPKNLSTGVNEGKKMRCEMDGR 150
QY 159 HGETFLHTNYSLKTKLRWYGODNTCEHYHTVGPISHCI PKDLALFTPEIWEATNRLGS 218
Db 151 --ETHELTNTLSEKMATHKFADCKAKRDT--PTSCIVDSTVYFVNIIEVVEALNALGK 206
QY 219 ARBQVLTLDLIDVYTTTPPPVNHVSRRVGLLEDQLSVWVSPALKDLPQAKYQIRRV 278
Db 207 VTSDHINFDVYKPKPPNHLVYNSEELSTIKLTWTN-PSIKSVIT-LKNIQYRTK 264
QY 279 DSDVMKVY---DVSNOTSCRLAGLKPGTVYFVOVRCNPFGIYSGKAGIWESEHPTAA 335
Db 265 DASTWSCIPEEDTASTSSFFVQDLKPFTEYVFRIR-----MEDDKGIVMSDSEASG 319
QY 336 STPSERP 343
Db 320 IT-YEDRP 326

RESULT 5

glycoprotein 130 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I49499, I48370
R:Salto, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130
A:Reference number: I48370, MUID:92291532, PMID:1602143
A:Accession: I49699
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RSS>
A:Cross-references: UNIPROT:Q00560; GB:M83336; NID:9193591; PIDN:AAA37723.1; PID:9193592
A:Accession: I48370
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RE2>
A:Cross-references: EMBL:X62646; NID:9840816; PIDN:CAA44515.1; PID:9840817
C:Genetics:
A:Gene: gp130
C:Keywords: glycoprotein
F:134-314/Domain: cytokine receptor homology <CRS>

Query Match 13.9%; Score 317.5; DB 2; Length 917;
Best Local Similarity 29.6%; Pred. No. 1.2e-16;
Matches 92; Conservative 50; Mismatches 146; Indels 23; Gaps 10;

QY 42 ISPDPTLLIGSSILATCSVHG--DPPGATBGLVYTLNGRRLPPELSRYLNASTLALA 98
Db 31 IYEPFPVVGSGNSFTATCVLKEACLOHYVNASYIWKTNAAVPREQVTVINNTTSVT 90
QY 99 LANINGSRQSGDNLVCHARDGSLAGSCLVYGPPEKPVNISCSKMKMDLTCRWPGA 158
Db 91 FTDLASINIGLTCNLTLPFGLEQNVYGITIISGLPPEKPKNLSTGVNEGKKMRCEMDGR 150
QY 159 HGETFLHTNYSLKTKLRWYGOD-NTCEHYHTVGPISHCI PKDLALFTPEIWEATNRLG 217
Db 151 --ETHELTNTLSEKMATHKFADCKAKRDT--PTSCIVDSTVYFVNIIEVVEALNALGK 203
QY 219 ARBQVLTLDLIDVYTTTPPPVNHVSRRVGLLEDQLSVWVSPALKDLPQAKYQIRRV 277
Db 207 VTSDHINFDVYKPKPPNHLVYNSEELSTIKLTWTN-PSIKSVIT-LKNIQYRTK 264
QY 279 DSDVMKVY---DVSNOTSCRLAGLKPGTVYFVOVRCNPFGIYSGKAGIWESEHPTAA 335
Db 265 DASTWSCIPEEDTASTSSFFVQDLKPFTEYVFRIR-----MEDDKGIVMSDSEASG 319
QY 336 STPSERP 343
Db 320 IT-YEDRP 326

RESULT 6

prolactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50455
R:Chen, X.; Horeman, N.D.
Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
A:Reference number: I50455, MUID:94283267, PMID:7516866
A:Accession: I50455
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CHB>
A:Cross-references: UNIPROT:Q00374; EMBL:U07694; NID:9466381; PIDN:AAA20646.1; PID:9466
F:36-220/Domain: cytokine receptor homology <CRS1>
F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match 13.8%; Score 316; DB 2; Length 830;
Best Local Similarity 36.6%; Pred. No. 1.4e-16;
Matches 75; Conservative 30; Mismatches 82; Indels 18; Gaps 8;

QY 133 PPEKPVNISCSKMKMDLTCRWPGAHGETFLH-TNYSLKTKLRWYGODNTCEHYHTGP 191
Db 231 PPEKPTIKRSPBKEFTFCMKKPGSDG--HPTVTLTYSKEGSERYVECPDYKTAGP 287
QY 192 HSCHI-PKDLALFTPEIWEATNRLGARSVDLTLDVTTDPPDV--HVSRYGL 248
Db 288 NSCFPDKHYSFWTIYITVKAINEIGSNVSDPLYVDVTVYVQTDPPVNTLEKKTNR 347
QY 249 EDQLSVRWSPPLKDP--LFOAKYQIRRVSDSDVMKVVDVSNOTSCRLAGLKPGTV 305
Db 348 KPYLVLTW-SPPPLADRSGLTLDYELRLKPEABEWET-FVGOQTHYKPSLNGKK 405
QY 306 YFVQVRCNPFGIYSGKAGIWESEMS 330
Db 406 YIVQIHCKP-----DHGSMSEMS 424

RESULT 7

interleukin-6 signal transducing molecule gp130 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44257
R:Mang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducin
A:Reference number: A44257, MUID:93052397, PMID:1427893
A:Accession: A44257
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <MAN>
A:Cross-references: UNIPROT:P40190
A:Experimental source: liver
A:Note: Sequence extracted from NCBI backbone (NCBI:118488)
C:Keywords: transmembrane protein
F:134-315/Domain: cytokine receptor homology <CRS>

Query Match 13.7%; Score 314.5; DB 2; Length 918;
Best Local Similarity 29.7%; Pred. No. 2e-16;
Matches 93; Conservative 51; Mismatches 140; Indels 29; Gaps 11;

QY 42 ISPDPTLLIGSSILATC-----SVHGDPGATBGLVYTLNGRRLPPELSRYLNAST 94
Db 31 IYEPFPVVGSGNSFTATCVLKEACLOVY-----SVNATYIWKTNHAAVPEQVTVINRTA 86
QY 95 LALANLNGSRQSGDNLVCHARDGSLAGSCLVYGPPEKPVNISCSKMKMDLTCRW 154
Db 87 SSVTFDVVQNTQVLTNLTLSFGQIEQNVYGITIISGLPPEKPKNLSTGVNEGKKMRCEMDGR 146
QY 155 TPQAHGETFLHTNYSLKTKLRWYGOD-NTCEHYHTVGPISHCI PKDLALFTPEIWEAT 213

D _b	147	D _B G-R-ETYLETNTTLKSE--WATEKEPDCCTKH--GTSSCMGTYTPFYFNITISWEAE	200
Q _y	214	NRLGSANSDVLTLLDLVVTTPPPDVHVSFVGLEDQLSVRWSPPALKDOLFQAKYQI	273
D _b	201	NALGNVNSEPTNFPDPVKVPSPPHNLSTVNSEELSLIKLAWNGL--DSILRLSDI	258
Q _y	274	RYYRVEDVDWKV---DDVSNQTSCLRLAGPGGVYFVQVCNPFGIYSGSKAGIWSEM	330
D _b	259	QYRKQASMTVIQVLELDIVTSPTSFYVDLKFPEIFYPRIR----SIKENCK-GYNWDMS	313
Q _y	331	HPTAASTPRSERP	343
D _b	314	E-EASGTTVEDRP	325

RESULT 8
A29884
prolactin receptor precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1989 #sequence, revision 30-Sep-1989 #text, change 09-Jul-2004
C/Accession: A29884
R/Bouthin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shirota, M.; Banville,
Cell 53, 69-77, 1988
A/Title: Cloning and expression of the rat prolactin receptor, a member of the growth ho
A/Reference number: A29884; MUID:8816059; PMID:2832068
A/Accession: A29884
A/Molecule type: mRNA
A/Residues: 1-310 <BOU>
A/Cross-references: UNIPROT:P05710; GB:M19304; NID:G206364; PIND:AAA41937.1; PID:G206365
C/Keywords: transmembrane protein
F/1-19/Domain: signal sequence
F/20-310/Product: prolactin receptor #status predicted <SIG>
F/31-216/Domain: cytokine receptor homology <CRS>

[illegible]

RESULT 9
A41070
prolactin receptor Nb2 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Jun-1992 #sequence_revise 12-Jun-1992 #text_change 09-Jul-2004
C;Accession: A41070; 155417
R;Ali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A;Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolactin
A;Reference number: A41070; MUID:92041834; PMID:1718958
A;Accession: A41070
A;Molecule type: mRNA
A;Residues: 1-412 <Ali>
A;Cross-references: UNIPROT:P05710; GB:M74152; NID:g206389; PIDN:AAA41946.1; PID:g206390
R;O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A;Title: Differential signal transduction of the short, Nb2, and long prolactin receptor

A:Reference number: I55417; MUID:95014432; PMID:7929319
 A:Accession: I55417
 A:Status: translated from GB/EMBL/DDDB
 A:Molecule type: mRNA
 A:Residues: 1-112 <R>
 A:Cross-references: EMBL:U07567; NID:g641963; PID:AAA61784.1; PID:g641964
 A:Experimental source: NB2-11C cell line
 C:Keywords: transmembrane protein
 F:31-216/Domain: cytokine receptor homology <C>

Query	March	13.7#;	Score 113;	DB 2;	Length 412;
Best Local Similarity	35.0#;	Pred. No. 9.9e-17;			
Matches	79;	Conservative 36;	Mismatches 85;	Indels 26;	Gaps 10;
QY	121	SILAGSCLYGLPREPEKPVNISCSWKNKMDLTCRWTPGAHGETFLHTNYSLKYLKWQGD	180		
DB	15	SILAGQS-----PQKDEIHKCRSPDKDXTFCWNNPGDGG--LPTNYSLTYSKE--GEK	65		
QY	181	NT--CEEHTWYGRHSCHPRD-LALFTRPYELWENATRLGSRARDVLTLDLDVYTTDPR	237		
DB	66	TTYECPDKXTSGNPSCFPSKQYTSIWMKIYIITVNAKTMQSSSDPLVDVDTYIVLEPPEP	125		
QY	238	PDVAVSRVYGLDEDLSTWAV--SPPALKDF---LFOAKYQIIRYVEDSVDMKVDVDSNQ	292		
DB	126	RNLRL- EYKQAKDKKTYLWVMKSPFLITDVTQWGMFTMEIRLRLPEAEKEHE- IHTFCHQ	183		
QY	293	TSCRLAGLKPGTTFVVOVRCNPFGLYSSKKAIGISENSHPAASTP	338		
DB	184	TOFVFFDLPGQKLYVOTRCKP-----DHGVSRMSQESSEVMP	222		

RESULT 10
A34631
lactogen receptor 1 - rat
C|Species: Rattus norvegicus (Norway rat)
C|Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C|Accession: A34631
R|Zhang, R.; Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
Biochem. Biophys. Res. Commun. 168, 415-422, 1990
A|Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA
A|Reference number: A34631, MUID:90241201, PMID:2159231
A|Accession: A34631
A|Status: Preliminary
A|Molecule type: mRNA
A|Residues: 1-610 <ZHA>
A|Cross-references: UNIPROT:P05710; GB:M4083; NID:G205122; PIDN:AAA79273.1; PID:G2051223
A|Note: The authors translated the codon GAG for residue 533 as Gly
F/31-216/Domain: cytokine receptor homology <CRS>

Query Match	13.7%	Score 313	DB 2	Length 610
Best Local Similarity	35.0%	Pred. No. 1,66-16		
Matches	79	Conservative	36	Mismatches 85
				Indels 26
				Gaps 10
QY	121	SILAGSCLYGLPEKRPVNISCSNMKDLTCRWTPGAHGETFHTNYSLKYLKRWYGD	180	
				:
DB	15	SILKGS-----PEKPEIHKCRSPDKETFCWMPGTDG--LPTNYSILYSKE--GEK	65	
QY	181	NT--CEEHVYSPRSCHIRPD-LALFTFYELIWEATNLSGARSPVLTLDILDVYTTDP	237	
				:
DB	66	TTYEPDPTKTSGPSNCSFSPSKQYTSIWKYIITVNAITNMGSSSDPLVYDVYIYEPEP	125	
QY	238	PDVHVSRRGGLIEDOLSRVW--SPPALKDF--LFOAKYQIIRYREDSVDMEKVVYDVSNO	292	
				:
DB	126	RNLT-L-EKQAKDKKTYLWAKMSPTLITIDVKTGWTMEYELIRLKEBAEEMW-IPFTGQ	183	
QY	293	TSCRLAGLKPGTVYFVQVRCNPFGLYGSKKAGIWMSEWHPPLPAASTP	338	
				:
DB	184	TOFVFVDLYPGQKYLVTQCKP-----DGVYSRWQESSEVNP	222	

RESULT 11
A36116
prolactin receptor 2 precursor - rat

C/Species: Rattus norvegicus (Norway rat)
 C/Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
 C/Accession: A36116
 R/Shiota, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Edey, M.; Djiane, J.
 Mol. Endocrinol. 4, 1136-1143, 1990
 A/Title: Expression of two forms of prolactin receptor in rat ovary and liver.
 A/Reference number: A36116; MUID:91155946; PMID:2293022
 A/Accession: A36116
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-610 <SHI>
 A/Cross-references: UNIPROT:P05710; GB:M57668; NID:g206366; PID:AAA1938.1; PID:g206367
 F/31-216/Domain: cytokine receptor homology <CRS>

Query Match
 Best Local Similarity 35.0%; Pred. No. 1.6e-16;
 Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;

121 SLAGSLVGLPEPEKVNISCSKMKMDLTCRWTGAGHGFPLHTNYSKYKLRWYGD 180
 15 SLKKGQ-----PGKREIHKCRSPDKETFCMNPGLDGG--LPTNYSLYTSKE--GEK 65
 181 NT--CEHYHTVGPSCHIPD-LALFTPEIWEATNRLGARSVDLTLDLIVTTDP 237
 66 TTECPDYKTSGPSNCFSSKQYTSIMKIYITVNATNQMGSSSDPLVVDVYIYEPEP 125
 238 PDHVSRRVGLLEDLSRWV--SPALKDF--LFOAKQIQRVREDSVDMKVVDVDSNQ 292
 126 RNLTL-EVKQDKDKKTYLWAKMSPTTIDVKTGMFTWEYERLKEEAEDEE-IFHTGHQ 183
 293 TSGRLAKPGTVFVQRCNPFGIYGSKKAGIWEWSHPTAATP 338
 184 TQPKVPLVPGOKLVOTRCKP-----DHGYWRRSGESSVEMP 222

Db
 293 TSGRLAKPGTVFVQRCNPFGIYGSKKAGIWEWSHPTAATP 338
 184 TQPKVPLVPGOKLVOTRCKP-----DHGYWRRSGESSVEMP 222

RESULT 12
 177525
 prolactin receptor precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C/Accession: I77925
 R/Davis, J.A.; Linzer, D.I.H.
 Mol. Endocrinol. 3, 674-680, 1989
 A/Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A/Reference number: I57699; MUID:89261824; PMID:2725531
 A/Accession: I77925
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-292 <RES>
 A/Cross-references: UNIPROT:Q08501; GB:M22959; NID:g200481; PID:AAA39977.1; PID:g200482
 F/31-216/Domain: cytokine receptor homology <CRS>

Query Match
 Best Local Similarity 31.4%; Pred. No. 1.2e-16;
 Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

86 LSRVLNASTLALANLNGSRGRSGDNLVCHARGSLAASCLYGLPPEKPVNISGWSK 145
 1 MSSALAYMLLVLSLNGQS-----PGKPEIHKCRSP 34
 146 NMKDLTCRWTGAGHGFPLHTNYSKYKLRWYGDNT--CEHYHTVGPSCHIPD-LAL 202
 35 DKETFTCMNPGSDGG--LPTNYSLYTSKE--GEKNTYECPDYKTSGPSNCFSSKQYTSI 90
 203 FTPEIWEATNRLGARSVDLTLDLIVTTDPDPVHVSRRVGLLEDLSVRWVS--PP 260
 91 WKIYIITVNATNMGSSDPLVVDVYIYEPEPRRLTL-EVKQDKDKKTYLWAKMLP 149
 261 ALKDF--LFOAKQIQRVREDSVDMKVVDVDSNQTSCLAGLKPGRVTVVQRCNPF 317
 150 TIDVKTGMFTWEYERLKEEAEDEE-IFHTGHQTFKVFDDLPGOKLVOTRCKP--- 205
 318 YGSKKAGIWEWSHPTAATP 338

Db
 206 ----DHGYWRRSGQEKSEIIP 222

RESULT 13
 177524
 prolactin receptor precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C/Accession: I77524
 R/Davis, J.A.; Linzer, D.I.H.
 Mol. Endocrinol. 3, 674-680, 1989
 A/Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A/Reference number: I57699; MUID:89261824; PMID:2725531
 A/Accession: I77524
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-303 <RES>
 A/Cross-references: UNIPROT:Q08501; GB:M22958; NID:g200479; PID:AAA39976.1; PID:g20048
 F/31-216/Domain: cytokine receptor homology <CRS>

Query Match
 Best Local Similarity 31.4%; Pred. No. 1.3e-16;
 Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

86 LSRVLNASTLALANLNGSRGRSGDNLVCHARGSLAASCLYGLPPEKPVNISGWSK 145
 1 MSSALAYMLLVLSLNGQS-----PGKPEIHKCRSP 34
 146 NMKDLTCRWTGAGHGFPLHTNYSKYKLRWYGDNT--CEHYHTVGPSCHIPD-LAL 202
 35 DKETFTCMNPGSDGG--LPTNYSLYTSKE--GEKNTYECPDYKTSGPSNCFSSKQYTSI 90
 203 FTPEIWEATNRLGARSVDLTLDLIVTTDPDPVHVSRRVGLLEDLSVRWVS--PP 260
 91 WKIYIITVNATNMGSSDPLVVDVYIYEPEPRRLTL-EVKQDKDKKTYLWAKMLP 149
 261 ALKDF--LFOAKQIQRVREDSVDMKVVDVDSNQTSCLAGLKPGRVTVVQRCNPF 317
 150 TIDVKTGMFTWEYERLKEEAEDEE-IFHTGHQTFKVFDDLPGOKLVOTRCKP--- 205
 318 YGSKKAGIWEWSHPTAATP 338
 206 ----DHGYWRRSGQEKSEIIP 222

Db
 318 YGSKKAGIWEWSHPTAATP 338
 206 ----DHGYWRRSGQEKSEIIP 222

RESULT 14
 153269
 prolactin receptor, long form - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C/Accession: I53269; J0671; S34356
 R/Claire, D.L.; Linzer, D.I.H.
 Endocrinology 133, 224-232, 1993
 A/Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.
 A/Reference number: I53269; MUID:93307149; PMID:8319571
 A/Accession: I53269
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-608 <RES>
 A/Cross-references: UNIPROT:Q08501; GB:L14811; NID:g293769; PID:AAA02686.1; PID:g29377
 R/Moore, R.C.; Oka, T.
 Gene 134, 263-265, 1993
 A/Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form
 A/Accession: J0671; MUID:94085788; PMID:8262385
 A/Accession: J0671
 A/Molecule type: mRNA
 A/Residues: 1-608 <MOO>
 A/Cross-references: GB:L13593; NID:g347398; PID:AA037641.1; PID:g347842
 R/Edey, M.; Pezet, A.; Nandi, S.; Kelly, P.A.
 submitted to the EMBL Data Library, June 1993
 A/Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.
 A/Reference number: S34356

A:Accession: S34356
A:Molecule type: mRNA
A:Residues: 1-557, 'F', 559-608 <EDB>
A:Cross-references: EMBL:X73712; NID:g312696; PIDN:CAA51789.1; PID:g312697
C:Comment: Prolactin receptor have long form and short form which are resulted from alternative splicing.
C:Comment: This long form receptor is capable of transducing a signal to milk protein gene.
C:Keywords: receptor; transmembrane protein
F:31-216/Domain: cytokine receptor homology <CRS>
F:230-253/Domain: transmembrane #status predicted <TM>

Query Match 13.5%; Score 309.5; DB 2; Length 608;
Best Local Similarity 31.4%; Pred. No. 3e-16;
Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

QY 86 LSRVLAASLTALALALINGSRGRSGDNLVCHARDGSLIAGSCLYGLPPEKPNVISCWSK 145
DB 1 MSSALVYMLVLSISLNGQS-----PPKPEIHKCRSP 34
QY 146 NMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGODNT--CEBYHTVGPSCHI PKD-LAL 202
DB 35 DKHPTCWMNPGSDG--LPTNYSLYTSKE--GEKNYECPPDYKTSGPSNCFPSKQYTSI 90
QY 203 FTFPEIWEATNRLSGASDVLTLTDLVTTDPPDVHVSRYGDEDLVSRAWVS--PP 260
DB 91 WKIYIITVNAIVNMGSTSDPLYVDVYIYEPEPRNLTL-EVKQLKDKKTYLWVKMLPP 149
QY 261 ALKDF---LFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGLKPGTVYFVQRCNPFGI 317
DB 150 TITDVKTGMFTWEYELRLSEADEWE-IHFTGHQTFKVFDLPGQKYLVTQTRCP--- 205
QY 318 YGSKKAGIWEWSHPTRAATP 338
DB 206 ----DHGYWSRMGQEKSIETP 222

RESULT 15

JQ1655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JQ1655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA sequence
A:Reference number: JQ1655; MID:93075121; PMID:1445292
A:Accession: JQ1655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: UNIPROT:Q04594; DDBJ:D13154; NID:g222848; PIDN:BA02439.1; PID:g222848
A:Experimental source: kidney
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAT>
F:36-219/Domain: cytokine receptor homology <CRS1>
F:239-425/Domain: cytokine receptor homology <CRS2>
F:439-462/Domain: transmembrane #status predicted <TM>
F:59, 91, 100, 112, 132, 262, 303, 315, 335, 647, 701, 800/Binding site: carbohydrate (Asn) (covale

Query Match 13.4%; Score 308; DB 2; Length 831;
Best Local Similarity 34.6%; Pred. No. 5.8e-16;
Matches 75; Conservative 28; Mismatches 96; Indels 18; Gaps 8;

QY 133 PPEKPNISQWKNMCDLTCRWTPGAHGETFLH-TNYSKYKLRWYGODNTCEYHTVGP 191
DB 230 PPEKPTIIRKSPKETFCTWMPKGLDG--HPTNYTLISKEGBOYECPPDYTAGP 286
QY 192 HSCHI-PKDLALFTPEIWEATNRLSGASDVLTLTDLVTTDPPDV--HVSRYGGL 248
DB 287 NSCYFPDKHGSFTIINITRAINEMGSNSDPHYVDVYIYQDPFPVNTLELKKPINR 346
QY 249 EDOLSVRAWVSPPALKDF---LFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGLKPGTV 305
DB 347 KPYLVLTW--SPPLADVRSGLTLIEYELRLKPEEGEWEI-FVGOOTQYKMFSLNPGKK 404

QY 306 YFVQRCNPFGIYGSKKAGIWEWSHPTRAATPRAER 342
DB 405 YIIQIHCKP-----DHGWSWSESENYYIQIPNDFR 435

Search completed: February 24, 2005, 03:36:50
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 24, 2005, 03:25:17 ; Search time 172 Seconds
(without alignments)
1253.403 Million cell updates/sec

Title: us-09-037-657-44

Perfect score: 2290

Sequence: 1 MPAGRGPAQASARPPPL.....NODEGILPGRGRTAGPAR 421

Scoring table: BLOSUM62

dapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2279.5	99.5	422	1	CRL1_HUMAN
2	2178	95.1	425	1	CRL1_MOUSE
3	1418.5	61.9	389	2	O6DG28
4	1384.5	60.5	394	2	O6UN05
5	365.5	16.0	918	2	O9W6U9
6	354	15.5	881	2	O57519
7	333	14.5	268	2	O8TD78
8	332	14.5	288	2	O96P36
9	332	14.5	349	2	O9UH45
10	332	14.5	376	2	O96P35
11	332	14.5	622	1	PRLR_HUMAN
12	327.5	14.3	1010	2	O7TQ89
13	325.5	14.1	206	2	O16354
14	323	14.1	918	1	IL6B_HUMAN
15	317.5	13.9	917	2	IL6B_MOUSE
16	317.5	13.9	917	2	O6PDI9
17	317	13.8	622	2	O9N0J7
18	316	13.8	622	1	PRLR_COLL1
19	315	13.8	622	2	O865V4
20	314.5	13.7	918	1	IL6B_PAT
21	313	13.7	610	1	PRLR_PAT
22	309.5	13.5	292	2	O8CTG1
23	309.5	13.5	581	1	PRLR_SHEEP
24	309.5	13.5	608	1	PRLR_MOUSE
25	309.5	13.5	608	2	O99JZ1
26	308	13.4	460	2	O7TQZ0
27	308	13.4	625	1	PRLR_PIG
28	308	13.4	831	1	PRLR_CHICK
29	308	13.4	831	2	O6QDA0
30	307	13.4	831	1	PRLR_MEIGA
31	306.5	13.4	581	1	PRLR_BOVIN

32	304	13.3	581	1	PRLR_CEREL	O28235 cervus elap
33	300.5	13.1	616	1	PRLR_RABIT	P14787 oryctolagus
34	294	12.8	611	2	O9PTI9	O9PTI9 xenopus lae
35	292.5	12.8	611	2	O9IBP6	O9IBP6 xenopus lae
36	292.5	12.8	611	2	O9PTI0	O9PTI0 xenopus lae
37	291.5	12.7	604	2	O6UAP8	O6UAP8 tetraodon n
38	291	12.7	870	2	O6UANO	O6UANO tetraodon n
39	290	12.7	626	2	O90WG7	O90WG7 cynops pyr
40	290	12.7	819	2	O6IEF7	O6IEF7 eublepharis
41	281.5	12.3	617	2	O75821	O75821 rana catesb
42	279.5	12.2	402	2	O7T121	O7T121 brachydanio
43	270.5	11.8	227	2	O9GLW3	O9GLW3 ursus marit
44	270.5	11.8	346	2	O9J404	O9J404 oreochromis
45	270.5	11.8	625	2	O9X892	O9X892 trichosurus

ALIGNMENTS

RESULT 1
CRL1_HUMAN STANDARD; PRT; 422 AA.
AC O75462; Q9UHS5;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Cytokine receptor-like factor 1 precursor (Cytokine-like factor-1)
DE (CLF-1) (Zcyto5) (UNQ288/PRO327).
GN Name=CRL1; Synonyms=ZCYTOR5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A., SUBUNIT, SUBCELLULAR LOCATION, TISSUE SPECIFICITY,
RP AND INDUCTION.
RC TISSUE=Fetal lung;
RX PubMed=9686600;
RA Elson G.C.A., Graber P., Loebinger C., Herren S., Gretener D.,
RA Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.-F.,
RT "Cytokine-like factor-1, a novel soluble protein, shares homology with
RL members of the cytokine type I receptor family.",
RL J. Immunol. 161:1371-1379(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Magrangeas F., Jacques Y., Minvielle S.,
RT "Cloning and expression of a novel soluble protein containing
RL hematopoietic cytokine receptor domains.",
RN Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Lok S., Prensell S.R., Jellmeberg A.C., Gilbert T., Whitmore T.E.,
RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.,
RN Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22867286; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Choi C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu O., Hase P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seasholtz S., Simmons L., Singh U., Smith V., Stinson J., Vagts A.,
RA Vanden R., Watanabe C., Wileand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RN "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.",
RN Genome Res. 13:2265-2270(2003).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;

RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins J.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Murty D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences,"
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
RP SEQUENCE OF 38-52.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.,
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites,"
RL Protein Sci. 13:2819-2824(2004).
[7]
RP INTERACTIONS WITH CLC AND CNTRF.
RX PubMed=1096616; DOI=10.1038/78765;
RA Elson G.C.A., Lelievre E., Guillet C., Chevalier S., Plun-Favreau H.,
RA Froger J., Suard I., de Coignac A.B., Delneste Y., Bometoy J.Y.,
RA Gauchat J.-F., Gascan H.,
RT "CLF associates with CLC to form a functional heteromeric ligand for
RT the CNTRF receptor complex,"
RL Nat. Neurosci. 3:867-872(2000).
[8]
RP VARIANTS C1SS HIS-81 AND ARG-374.
RX PubMed=12509788;
RA Knappskog P.M., Majewski J., Llynech A., Nilsen P.T.E., Bringsall J.S.,
RA Ott J., Boman H.,
RT "Cold-induced sweating syndrome is caused by mutations in the CRPL1
RT gene,"
RL Am. J. Hum. Genet. 72:375-383(2003).
CC -1- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory
CC role in the immune system and during fetal development. May be
CC involved in nervous system development.
CC -1- SUBUNIT: Forms covalently linked di- and tetramers. Forms a
CC heteromeric complex with cardiotrophin-like cytokine (CLC); the
CC CRPL1/CLC complex is a ligand for the ciliary neurotrophic factor
CC receptor (CNTRF).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Highest levels of expression observed in
CC spleen, thymus, lymph node, appendix, bone marrow, stomach,
CC placenta, heart, thyroid and ovary. Strongly expressed also in
CC fetal lung.
CC -1- INDUCTION: Up-regulated in fibroblast primary cell cultures under
CC stimulation by IFN-gamma, TNF-alpha and IL-6.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -1- DISEASE: Defects in CRPL1 are the cause of cold-induced sweating
CC syndrome (C1SS) [MIM:272430]. C1SS is an autosomal recessive
CC disorder characterized by profuse sweating induced by cool
CC surroundings (temperatures of 7 to 18 degrees Celsius). Additional
CC abnormalities include a high-arched palate, nasal voice, depressed
CC nasal bridge, inability to fully extend the elbows and
CC hypohidrosis.
CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 3.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

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CC or send an email to license@sib-sib.ch).
DR EMBL; AF059293; AAC28335.1; -
DR EMBL; AF073515; AAD39681.1; -
DR EMBL; AF178684; AAD54385.1; -
DR EMBL; AY58291; AAO88658.1; -
DR EMBL; BC044634; AAH44634.1; -
DR HSSP; P40223; 1C09.
DR Genew; HGNC:2364; CRPL1.
DR MIM; 604237; -
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS50835; IG_LIKE; FALSE NEG.
KW Direct protein sequencing; Disease mutation; Glycoprotein;
KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal.
FT SIGNAL 1 37
FT CHAIN 38 422 Cytokine receptor-like factor 1.
FT DOMAIN 38 131 Ig-like C2-type.
FT DOMAIN 134 229 Fibronectin type-III 1.
FT DOMAIN 234 334 Fibronectin type-III 2.
FT SITE 327 331 WSXWS motif.
FT DISULFID 143 153 By similarity.
FT DISULFID 184 195 Phosphoserine (By similarity).
FT MOD RES 219 219 N-linked (GlcNAc...) (potential).
FT CARBOHYD 92 92 N-linked (GlcNAc...) (potential).
FT CARBOHYD 104 104 N-linked (GlcNAc...) (potential).
FT CARBOHYD 140 140 N-linked (GlcNAc...) (potential).
FT CARBOHYD 168 168 N-linked (GlcNAc...) (potential).
FT CARBOHYD 292 292 N-linked (GlcNAc...) (potential).
FT CARBOHYD 382 382 N-linked (GlcNAc...) (potential).
FT VARIANT 81 81 R -> H (1n C1SS).
FT VARIANT 374 374 /FTID=VAR_017865.
FT VARIANT 374 374 L -> R (1n C1SS).
FT CONFLICT 240 240 /FTID=VAR_017866.
FT CONFLICT 422 422 D -> E (1n Ref. 3).
SQ SEQUENCE 422 AA; 46301 MW; AD9DEFCEB01B84228 CRC64;
Query Match 99.5%; Score 2279.5; DB 1; Length 422;
Best Local Similarity 99.8%; Pred. No. 7.1e-165;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MPAGRGPAAGSARRPPLLP-LLLLCTVGAPRAGGATTAVISPDPPTLLIGSSILATC 59
QY 1 MPAGRGPAAGSARRPPLLP-LLLLCTVGAPRAGGATTAVISPDPPTLLIGSSILATC 60
DB 1 MPAGRGPAAGSARRPPLLP-LLLLCTVGAPRAGGATTAVISPDPPTLLIGSSILATC 60
QY 60 SVHGDPPGATAGLWYTLNGRRLPELSRVLNASTLATLANVINGSRGSGNLYCHAD 119
DB 61 SVHGDPPGATAGLWYTLNGRRLPELSRVLNASTLATLANVINGSRGSGNLYCHAD 120
QY 120 GSTLASCTLYGLPEPKPNVICSWNMKDLTCRWTPGAGHGTPLHTNYSLKTKLRWYQ 179
DB 121 GSTLASCTLYGLPEPKPNVICSWNMKDLTCRWTPGAGHGTPLHTNYSLKTKLRWYQ 180
QY 180 DNTCEHYHTVGPSCCHIKPOLALFTPEYIWEATNRLSGARSADVLTLIDLVTTDPPD 239
DB 181 DNTCEHYHTVGPSCCHIKPOLALFTPEYIWEATNRLSGARSADVLTLIDLVTTDPPD 240
QY 240 VHSRVGLEGDLSRVWSPALIKDPLFOAKYQIRYVEDSVDMKVVDVSNQTSCLAG 299

DB 241 VHSRVSGLLEDQSVSWSPALKDPLFOAKYQIRRVEDSVWVKVVDVSNQTSCLAG 300
QY 300 LKRGTYFVQVVRNPNPGIYSSKAGIWSHSHPTASTPSSRPGGACGCRGGPSS 359
DB 301 LKRGTYFVQVVRNPNPGIYSSKAGIWSHSHPTASTPSSRPGGACGCRGGPSS 360
QY 360 GPRVRELKQPLGLMKHAYCSNLSFRLYDQWRAMQSKHTRNODGILPSGRGRTARGP 419
DB 361 GPRVRELKQPLGLMKHAYCSNLSFRLYDQWRAMQSKHTRNODGILPSGRGRTARGP 420
QY 420 AR 421
DB 421 AR 422
RESULT 2
CRL1_MOUSE STANDARD; PRT; 425 AA.
ID CRL1_MOUSE
AC 09JUN8;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-JUN-2005 (Rel. 46, Last annotation update)
DE Cytokine receptor-like factor 1 precursor (Cytokine-like factor-1)
DE (CLF-1) (Cytokine receptor-like molecule 3) (CRLM-3) (NR6).
GN Name=Crlf1; Synonyms=Crlm3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RX [1]
RP SEQUENCE FROM N.A.
RL Hitroyama T., Iwama A., Nakamura Y., Nakauchi H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RN FUNCTION, AND TISSUE SPECIFICITY.
RX PubMed=10359701; DOI=10.1016/S0960-9822(99)80266-8;
RA Alexander W.S., Rakar S., Robb L., Farley A., Willson T.A.,
RA Zhang J.-G., Hartley L., Kikuchi Y., Kojima T., Nomura H.,
RA Hasegawa M., Maeda M., Faderl L., Jachno K., Nash A., Metcalfe D.,
RA Nicola N.A., Hilton D.J.;
RA "Suckling defect in mice lacking the soluble haemopoietin receptor
NR6";
RL Curr. Biol. 9:605-608(1999).
RN [3]
RN PHOSPHORYLATION SITE SER-222.
RX PubMed=15378723; DOI=10.1002/jcm.1604;
RA Jin W.H., Dai J., Zhou H., Xia O.C., Zou H.F., Zeng R.;
RT "Phosphoproteome analysis of mouse liver using immobilized metal
affinity purification and linear ion trap mass spectrometry";
RL Rapid Commun. Mass Spectrom. 18:2169-2176(2004).
CC -1- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory
CC role in the immune system and during fetal development. May be an
CC essential role in the initiation and/or maintenance of suckling in
CC neonatal mice.
CC -1- SUBUNIT: Forms covalently linked di- and tetramers. Forms a
CC heteromeric complex with cardiotrophin-like cytokine (CLC); the
CC CRL1/CLC complex is a ligand for the ciliary neurotrophic factor
CC receptor (CNTFR) (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- TISSUE SPECIFICITY: Widely expressed in the embryo. Not detected
CC in the brain of adult mice.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 3.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>
CC or send an email to license@1sb-sib.ch).

DR EMBL; AB040038; BAA92777.1; -
DR HSSP; P40223; 1CD9.
DR MGD; MGI:1340030; Crlf1.
DR InterPro; IPR002996; Cyt_kn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; IG_III-like.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS50835; IG_Like; FALSE_NEG.
KM Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;
KM Repeat; Signal.
FT SIGNAL 1 33
FT CHAIN 34 425
FT DOMAIN 35 134
FT DOMAIN 137 232
FT DOMAIN 237 337
FT SITE 330 334
FT SITE 330 334
FT DISULFID 146 156
FT MOD_RES 187 198
FT MOD_RES 222 222
FT CARBOHYD 95 95
FT CARBOHYD 107 107
FT CARBOHYD 143 143
FT CARBOHYD 171 171
FT CARBOHYD 295 295
FT CARBOHYD 385 385
SQ SEQUENCE 425 AA; 46662 MW; 910535629CA7056 CRC64;
Query Match 95.1%; Score 2178; DB 1; Length 425;
Best local Similarity 94.8%; Pred. No. 3 7e-157;
Matches 402; Conservative 5; Mismatches 13; Indels 4; Gaps 2;
QY 1 MPARRRGPAQAASARRP-PLPLP---LLLCVIGAPRAGGAAHTAVISPDPTLLIGSSLL 56
DB 1 MPARRRGPAQAASARRPPLPLSLMSPLLCVIGAPRAGGAAHTAVISPDPTLLIGSSLL 60
QY 57 ATCSVHGDPGPAATAGLYTTTLNRRRLPPELSRYLANSTALALANLNGSRQSGDNLVCH 116
DB 61 ATCSVHGDPGPAATAGLYTTTLNRRRLPPELSRYLANSTALALANLNGSRQSGDNLVCH 120
QY 117 ARDGSILASCLVYGLPPEKPVNISQWSKMDLTCRWTPGAHGETFLHTNYSLKTKLR 176
DB 121 ARDGSILASCLVYGLPPEKPVNISQWSKMDLTCRWTPGAHGETFLHTNYSLKTKLR 180
QY 177 YGQDNTCEEHYTVGPSPHSCHI PKDLALFTPEYIWEATNLSARSVDLTLDLVVTTDP 236
DB 181 YGQDNTCEEHYTVGPSPHSCHI PKDLALFTPEYIWEATNLSARSVDLTLDLVVTTDP 240
QY 237 PPDVHSRVVGLLEDQSVSWSPALKDPLFOAKYQIRRVEDSVWVKVVDVSNQTSCLAG 296
DB 241 PPDVHSRVVGLLEDQSVSWSPALKDPLFOAKYQIRRVEDSVWVKVVDVSNQTSCLAG 300
QY 297 LAGLKRGTYFVQVVRNPNPGIYSSKAGIWSHSHPTASTPSSRPGGACGCRGGPSS 356
DB 301 LAGLKRGTYFVQVVRNPNPGIYSSKAGIWSHSHPTASTPSSRPGGACGCRGGPSS 360
QY 357 PPSGPRVRELKQPLGLMKHAYCSNLSFRLYDQWRAMQSKHTRNODGILPSGRGRTARGP 416
DB 361 PPSGPRVRELKQPLGLMKHAYCSNLSFRLYDQWRAMQSKHTRNODGILPSGRGRTARGP 420
QY 417 RGPA 420
DB 421 RGPA 424

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RESULT 3
Q6DG28 PRELIMINARY; PRT; 389 AA.
ID Q6DG28
AC Q6DG28;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Zgc:91992.
GN Name=zgc:91992.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
OK NCB1
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scherz T.E.,
RA Brownstein M.J., Uedin T.B., Teshnyki S., Carninci P., Prange C.,
RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mallary S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.;
RX Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL: BC076526; AAH76526.1; -
DR InterPro: IPR002996; Cytkn_recept_B/G.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS50853; FN3; 2.
SQ SEQUENCE 389 AA; 43314 MW; E30903B99639864A CRC64;

Query Match 61.9%; Score 1418.5; DB 2; Length 389;
Best Local Similarity 67.6%; Pred. No. 1.7e-99;
Matches 261; Conservative 50; Mismatches 70; Indels 5; Gaps 4;
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DB 240 PPALDPLFQAKYQIRYRVEDSDVMKVVDVSNQTSCLGLKPGTVYFVQVRCNPGIY 318
QY 319 GSKKAGIWEWSHPAASTPNSERPFGGACERPGEBSGPVRELKQIFGMLKRAY 378
DB 300 GSRKAGISDWSHPAASTPNSERFLT--GSCDSKAGQONS-TLRBDIKQFGWVRKRAY 356
QY 379 -CSNLSFRLYDQWRAMQKSHKTRNQ 403
DB 357 GSGMSIKLYDQWRVWLQKSHKTRNQ 382

RESULT 4
Q6UA05 PRELIMINARY; PRT; 394 AA.
ID Q6UA05
AC Q6UA05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Claes I helical cytokine receptor number 1.
GN Name=CRPAl;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
NCBI_TaxID=99883;
OK NCB1
RN [1]
RP SEQUENCE FROM N.A.
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Strange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozou-Costas C., Bernot A.,
RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Antouard V., Jubin C., Caetelli V., Katinka M., Vacherie B.,
RA Blumont C., Skalli Z., Catolico L., Poulain V., Berardins Vd.,
RA Crnaud C., Duprat S., Broctier P., Coutanceau J.-P., Gouzy U.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McSwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigs R., Zody M.C., Meisrov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laude V., Schachter V., Quittier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach U., Collins H.R.;
RT "Analysis of the Tetraodon nigroviridis genome reveals the
RT prokaryocyte of bony vertebrates and its duplication in teleost
RT fish.";
RL Nature 0:0-0(2004).
DR EMBL: AY374473; AAR25664.1; -
GO GO:0004872; F1:receptor activity; IEA.
DR InterPro: IPR002996; Cytkn_recept_B/G.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR007110; Ig-like.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS50853; FN3; 2.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Receptor.
SQ SEQUENCE 394 AA; 44022 MW; EE60B16FA2C2896C CRC64;

Query Match 60.5%; Score 1384.5; DB 2; Length 394;
Best Local Similarity 67.6%; Pred. No. 6.6e-97;
Matches 259; Conservative 41; Mismatches 78; Indels 5; Gaps 4;
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Oy		202	FTPEIWEATNRIGSARSDVLTLDIDVTTPDPDVHSRVGLEQOLSVRWSPBPA	261
Dd		188	LFTPEIWEASNOGRATSVDITLDDIVDTTDPDPSGVTVSRVQOLEQOLSVRWAEAPPA	247
Oy		262	LKDLFLQAKYQIRVRVEDSDVKWVDVDSNQTSCRLAGLKPGTYVFVQVRCNPFGISGSK	321
Dd		248	LKDPLFAQKYQRRLYLEDSDQWKWDVDVGNQTSCLAGLRPGTYVFVQVRCNPVGIYGSR	307
Oy		322	KAGTWSEWSHPAASTPPSERGGCGACERPFGSSGPVARELKOPLGLMKRAY-CS	380
Dd		308	KAGTWSEWSHPAASTPPSER--LMWGSGCDSSXADSNSTYLRELKOPFGGWKRKAAYCS	365
Oy		361	NLSFRLYDQMPRAMQSHKTRNQ	403
Dd		366	SMSMKTLYDQMRVLMQSHKARANQ	388
 RESULT 5				
ID	Q9W6U9	PRELIMINARY;	PRT;	918 AA.
AC	Q9W6U9.			
DT	01-NOV-1999	(TREMBLrel. 12,	Created)	
DT	01-NOV-1999	(TREMBLrel. 12,	Last sequence update)	
DT	01-MAR-2004	(TREMBLrel. 26,	Last annotation update)	
DE	Glycoprotein 130 precursor.			
GN	Name=gp130;.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Archaeosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OX	NCBI_Taxid=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Embryonic heart primary culture;			
RX	MEDLINE=9902608; PubMed=9806927;			
RA	Gelissen M., Heiller S., Pennica D., Ernberger U., Rohrer H.;			
RT	"The specification of sympathetic neurotransmitter phenotype depends			
RL	on gp130 cytokine receptor signaling.";			
DR	Development 125:4791-4801(1998).			
DR	EMBL; AJ011688; CAB42084.1; --			
DR	HSSP; P40189; IBCU.			
DR	InterPro; IPR002996; Cyt_kn_recept_B/G.			
DR	InterPro; IPR003961; FN_III.			
DR	InterPro; IPR008957; FN_III-like.			
DR	InterPro; IPR003529; Hemptrecept_1302.			
DR	InterPro; IPR010457; Lep_receptor_I9.			
DR	Pfam; PF00041; tn3; 4.			
DR	Pfam; PF06328; Lep_receptor_Ig; 1.			
DR	SMART; SM00060; FN3; 4.			
DR	PROSITE; PS00853; FN3; 5.			
DR	PROSITE; PS01353; HEMATOPO_REC_L_P2; UNKNOWN_1.			
KM	Signal.			
FT	SIGNAL.			
SO	SEQUENCE	1	26 Potential.	
		918 AA;	102495 MW; FE7625FFE3E313BF CRC64;	
	Query Match	16.0%;	Score 365.5; DB 2;	Length 918;
	Best Local Similarity	30.1%;	Pred. No. 5,1e-19;	
	Matches 102;	Conservative 44;	Mismatches 136;	Indels 57;
				Gaps 14
Oy		42	ISPDPTLLIGSSLATCSVHG---DPPGATAGLVWTNGRRLLPPELSRYVLNSTALALA	98
Dd		34	IIPESPVLATGSNFALCIINBSCHDFGNIVASQIIWMKKNKVIREQYREINRTVSVT	93
Oy		99	LANINGSORSSDNVCHA-RGSI---LAGCCLVGDLPREPVAISC-----WSK	145
Dd		94	FNDTSS----IASPLTCNVLAAGQEONITYGISVTGVPREPKNLSCTVIYISPVEXYM	149
Oy		146	NMKDILTCWTPGAHGETFLAHNTYSIKYKLRYGQONTCEBYHTVGPHSCHIPKDALFTP	205
Dd		150	N-----CWNPBRH--FTIDIRFRALKYMWKPRTFPDCIPEYN--NCTI-SDVQFEVN	198
Oy		206	YEIWVEATNRIGSARSADVLTLDIDVTTPDPDVHSRVGLEQOLSVRWSPBPA	265

[illegible]

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RESULT 7
Q8TD78      PRELIMINARY;      PRT;      268 AA.
ID 08TD78;
AC 08TD78;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Prolactin receptor delta 7/11.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Breast tumor;
RA Trotte J.F., Hovey R.C., Koduri S., Vonderhaar B.K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF492470; AAM18048.1; -.
DR HSSP; P16471; 1BP3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain..); IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytok_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; HemptreceptL_FL.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_FL; 1.
DR KMW Receptor.
SQ SEQUENCE 268 AA; 30705 MW; FBA98AB6A9A078C CRC64;

Query Match 14.5%; Score 333; DB 2; Length 268;
Best Local Similarity 36.6%; Pred. No. 3.3e-17;
Matches 83; Conservative 29; Mismatches 97; Indels 18; Gaps 8;

QY 122 ILAGSLTYVG-LPPEKPVNISCSKMKMDLTGRWTPGAHGETFLHTNYSLSKYLKRWYGD 180
DB 15 LFLNTCLINGQLPFGKPEIFKCRSPNKETFTCMWRGTG--LPTNYSLTYHREGETLM 72
QY 181 NTCEEYHTVGPSPCHIPKD-LALFTPYEIVWEATNRLGSARSVDLTLDIVVTTDPPD 239
DB 73 HECPTDITGPNSSCHFGKQYTMWRTYIMVNATNQMGSSFDELVDVYTYVQDDPPL 132
QY 240 VHVSRVGLIEDQLSVRWV--SPPALKDF--LFOAKYQIRYVEDSDVKVVDVSNQTS 294
DB 133 LAV-EVKQPEDRKPRYLIMKMSPTLLDLKTGWFTLLYEIRLKEKAWE-IFHAGQOTE 190
QY 295 CRLAGLKPGTVFYVQRCNPFGIYSGKAGIWESESHPTAASPRPS 341
DB 191 FKLSLHPQKYLVOYRCKP-----DHGYSAMSAPATITQIPSGD 230

RESULT 8
Q96P36      PRELIMINARY;      PRT;      288 AA.
ID 096P36;
AC 096P36;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Prolactin receptor short isoform 1b.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Placenta;
RA Trotte J.F., Hovey R.C., Vonderhaar B.K.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416618; AAL23914.1; -.

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DR PIR; B59405; B59405.
DR HSSP; P16471; 1BP3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain..); IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytok_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; HemptreceptL_FL.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_FL; 1.
DR KMW Receptor.
SQ SEQUENCE 288 AA; 32760 MW; B45203BC045EB417 CRC64;

Query Match 14.5%; Score 332; DB 2; Length 288;
Best Local Similarity 37.1%; Pred. No. 4.3e-17;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

QY 122 ILAGSLTYVG-LPPEKPVNISCSKMKMDLTGRWTPGAHGETFLHTNYSLSKYLKRWYGD 180
DB 15 LFLNTCLINGQLPFGKPEIFKCRSPNKETFTCMWRGTG--LPTNYSLTYHREGETLM 72
QY 181 NTCEEYHTVGPSPCHIPKD-LALFTPYEIVWEATNRLGSARSVDLTLDIVVTTDPPD 239
DB 73 HECPTDITGPNSSCHFGKQYTMWRTYIMVNATNQMGSSFDELVDVYTYVQDDPPL 132
QY 240 VHVSRVGLIEDQLSVRWV--SPPALKDF--LFOAKYQIRYVEDSDVKVVDVSNQTS 294
DB 133 LAV-EVKQPEDRKPRYLIMKMSPTLLDLKTGWFTLLYEIRLKEKAWE-IFHAGQOTE 190
QY 295 CRLAGLKPGTVFYVQRCNPFGIYSGKAGIWESESHPTAASPRPS 338
DB 191 FKLSLHPQKYLVOYRCKP-----DHGYSAMSAPATITQIP 227

RESULT 9
Q9UHJ5      PRELIMINARY;      PRT;      349 AA.
ID 09UHJ5;
AC 09UHJ5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Intermediate prolactin receptor isoform.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20054419; PubMed=10585417; DOI=10.1074/jbc.274.50.35461;
RA Kline J.B., Roehrs H., Clevenger C.V.;
RT "Functional characterization of the intermediate isoform of the human
RT prolactin receptor."
RL J. Biol. Chem. 274:35461-35468(1999).
DR EMBL; AF16329; AAD49855.1; -.
DR HSSP; P16471; 1BP3.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0042978; F:ornithine decarboxylase activator activity; NAS.
DR GO; GO:0004925; F:prolactin receptor activity; NAS.
DR GO; GO:0042803; F:protein homodimerization activity; NAS.
DR GO; GO:0006916; P:anti-apoptosis; NAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu..; NAS.
DR GO; GO:0007595; P:lactation; NAS.
DR GO; GO:0006964; P:steroid biosynthesis; NAS.
DR GO; GO:0042110; P:T-cell activation; NAS.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin..; IEA.
DR GO; GO:0042977; P:tyrosine phosphorylation of JAK2 protein; NAS.
DR InterPro; IPR002996; Cytok_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; HemptreceptL_FL.

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DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PSS0853; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor.
SQ SEQUENCE 349 AA; 39806 MW; 932F200E850CD27 CRC64;
Query Match 14.5%; Score 332; DB 2; Length 349;
Best Local Similarity 37.1%; Pred. No. 5.4e-17;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;
QY 122 ILAGSCLYVG-LPPEKPVNISCSKMKDLCRTWPGAHGETFLHTNYSLKYLKRWGQD 180
DB 15 LFLNTCLNLQQLPPGKREIFKCRSPNKETFTCWRRPCTDGG--LPNTYSLTYHREGFTLM 72
QY 181 NTCEBHTVTPHSGHAIKPD-LALFTPEYIWEATNRLGASRDVLTLDIDVTTDPPD 239
DB 73 HECPDYITGPNCHGKQYTSWMRTYIMVNATNMGSSFSDELIVDYVYIYQPPDPLE 132
QY 240 VHSRVGGLDQLSVRV--SPPALKDF---LFQAKYQIRYVEDSVDMKVVDVNSQTS 294
DB 133 LAV-EVQPEDRKPYLMIKWSPPTLIDLTGWFLLYEIRLKPEKAAEWB-IHPAGQOTE 190
QY 295 CRLAGLKPGTVYFVQVRCNPFGIYSGKKAGIWESESHPTAATP 338
DB 191 FKILSLHPGQKYLIVQVRCF-----DHGYWSMSPATFIQIP 227
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AC Q96P35;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Prolectin receptor short isoform 1a.
GN Name=PRLR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Trott J.F., Hovey R.C., Vonderhaar B.K.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF16619; AL23915.1; -
DR PIR; A59405; A59405.
DR HSSP; P16471; 1BP3.
DR GO; GO:0009866; C:cell surface; ISS.
DR GO; GO:0042378; F:ornithine decarboxylase activator activity; ISS.
DR GO; GO:0004925; F:prolactin receptor activity; ISS.
DR GO; GO:0042803; F:protein homodimerization activity; ISS.
DR GO; GO:0006916; P:anti-apoptosis; ISS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; ISS.
DR GO; GO:0007595; P:lactation; ISS.
DR GO; GO:0006694; P:steroid biosynthesis; ISS.
DR GO; GO:0042110; P:T-cell activation; ISS.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR InterPro; IPR002996; Cytok. recept. B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; Hemtreceptl_F1.
DR Pfam; SM00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PSS0853; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor.
SQ SEQUENCE 376 AA; 42639 MW; 112DC2555FBC4601 CRC64;
Query Match 14.5%; Score 332; DB 2; Length 376;
Best Local Similarity 37.1%; Pred. No. 5.9e-17;

Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;
QY 122 ILAGSCLYVG-LPPEKPVNISCSKMKDLCRTWPGAHGETFLHTNYSLKYLKRWGQD 180
DB 15 LFLNTCLNLQQLPPGKREIFKCRSPNKETFTCWRRPCTDGG--LPNTYSLTYHREGFTLM 72
QY 181 NTCEBHTVTPHSGHAIKPD-LALFTPEYIWEATNRLGASRDVLTLDIDVTTDPPD 239
DB 73 HECPDYITGPNCHGKQYTSWMRTYIMVNATNMGSSFSDELIVDYVYIYQPPDPLE 132
QY 240 VHSRVGGLDQLSVRV--SPPALKDF---LFQAKYQIRYVEDSVDMKVVDVNSQTS 294
DB 133 LAV-EVQPEDRKPYLMIKWSPPTLIDLTGWFLLYEIRLKPEKAAEWB-IHPAGQOTE 190
QY 295 CRLAGLKPGTVYFVQVRCNPFGIYSGKKAGIWESESHPTAATP 338
DB 191 FKILSLHPGQKYLIVQVRCF-----DHGYWSMSPATFIQIP 227
RESULT 11
PRLR_HUMAN STANDARD; PRT; 622 AA.
AC P16471; Q9BX87;
DT 01-AUG-1990 (Ref. 15, Created)
DT 01-AUG-1990 (Ref. 15, Last sequence update)
DT 25-OCT-2004 (Ref. 45, Last annotation update)
DE Prolectin receptor precursor (PRL-R).
GN Name=PRLR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=90114212; PubMed=2558309;
RA Boutin J.-M., Edey M., Shirota M., Jolicoeur C., Lesueur L., Ali S.,
RA Gould D., Djiane J., Kelly P.A.;
RT "Identification of a cDNA encoding a long form of prolactin receptor
RT in human hepatoma and breast cancer cells.";
RL Mol. Endocrinol. 3:1455-1461(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99182102; PubMed=10084611; DOI=10.1210/jc.84.3.1153;
RA Hu Z.-Z., Zhuang L., Meng J., Leonidree M., Dufat M.L.;
RT "The human prolactin receptor gene structure and alternative promoter
RT utilization: the generic promoter hplii and a novel human promoter
RT hpl(N).";
RL J. Clin. Endocrinol. Metab. 84:1153-1156(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Breast carcinoma;
RA Kline J.B., Clevenger C.V.;
RT "Characterization of a novel and functional human prolactin receptor
RT isoform (delta-S1 PRLr) containing only one extracellular fibronectin-
RT like domain.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Teshnyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

DT 01-MAR-2004; (TREMBlrel. 26, last annotation update)
 DE A01055.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OK NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Xu C.S., Li W.O., Li Y.C., Han H.P., Wang G.P., Chai L.O., Yuan J.Y.,
 RA Yang K.J., Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F.,
 RA Shi J.B., Raiman S., Wang Q.N., Zhang J.B.,
 RL Submitt (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY310138; AAP78746.1; -
 DR HSSP; P40189; 1B78.
 DR InterPro: IPR002996; Cytkn_recept_B/G.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-1like.
 DR Pfam; PF00041; fn3; 4.
 DR SMART; SM00060; FN3; 4.
 DR PROSITE; PSS0853; FN3; 4.
 SO SEQUENCE 1010 AA; 112942 MW; 78F3CE56C952DBD7 CRC64;

Query Match 14.3%; Score 327.5; DB 2; Length 1010;
 Best Local Similarity 30.0%; Pred. No. 4.5e-16;
 Matches 94; Conservative 51; Mismatches 139; Indels 29; Gaps 11;

QY 42 ISHPDPLILGSSILATC-----SYHGDPGATAGLTYTLNGRLPPELSVYLAAT 94
 DB 21 IYEPFVVGSGNSATATCVLKEKCLQYV---SVNATYIWKTHVAVPKEQVIVNRTA 76
 QY 95 LALALANLNGSRSGNGLVCHARDGSLIAGSCLYGLPREKPNVISCNMKDLQCRW 154
 DB 77 SSYTFDVVQNNQLTNIIISFGQIEQNVGITTLSGYPPIPNLSCYINEGKMLCOW 136
 QY 155 TPQAGETPLHTVSLKYLKRWYQD-NTCEHYHTVPHSCHLPKDLALFTPEIWEAT 213
 DB 137 DPGR--ETYLETVYTLKSE--WATEKPPDRKTH--GTSQCMQGYTFIYFANIEWVEAE 190
 QY 214 NRGASASDVLTLDLDVTTDPPDVHVRGGLQSLQSVKWSPPALDPLFOAKYQI 273
 DB 191 NALGNVSSSEPINDPVDKVPSPHNNISVNSELSILKLAWNQGL--DSIIRLSDI 248
 QY 274 RYRVEDSDVMKVV---DDVSNQTSCLRGLKPGTVYVQVRCNFGIYSGKKAGIWEWS 330
 DB 249 QYTKDASTYIQVPLEDTVSPTSFTVQDLKPTETVFRIR---SIKENGK-GYWSQWS 303
 QY 331 HPTAATPSESRP 343
 DB 304 E-EASGTTVEDRP 315

RESULT 13
 Q16354 PRELIMINARY; PRT; 206 AA.
 AC 016354;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
 DE Prolactin receptor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95286597; PubMed=7768908; DOI=10.1074/jbc.270.22.11133;
 RA Puh G., Wells J.A.;
 RT "Prolactin receptor antagonists that inhibit the growth of breast
 cancer cell lines."
 RL J. Biol. Chem. 270:11333-11337(1995).
 DR EMBL; S78505; AAB34470.1; -
 DR HSSP; P16471; 1BP3.

DR GO; GO:0016020; C:membrane, IEA.
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro: IPR002996; Cytkn_recept_B/G.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-1like.
 DR InterPro: IPR003528; Hemprecept_F1.
 DR Pfam; PF00041; fn3; 2.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PSS0853; FN3; 2.
 DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
 DR Kew Receptor.
 FT NON TER
 SO SEQUENCE 206 AA; 23950 MW; CED939781B3C804E CRC64;

Query Match 14.2%; Score 325.5; DB 2; Length 206;
 Best Local Similarity 37.6%; Pred. No. 8.8e-17;
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 DB 2 LPPEKPEIFKCRSPNKSTFTCMRPGTDG--LPTNYSLYHREGFTLMECPDYITGCP 59
 QY 192 HSGHIPKD-LALFTPEIWEATNRLGASASDVLTLDLDVTTDPPDVHVRGGLQ 250
 DB 60 NSCHFQGYQYTSMTRTYIMVNNATNQKSSFSDELVDVYTVIYQDPDLLEAV-EVKQPD 118
 QY 251 QLSVRVY--SPPAIKDF--LFOAKYQIRYRVEDSDVMKVVDDVSNQTSCLRGLKPGTV 305
 DB 119 RKPLVIMKSPPLTLDIKTGMFTLYIRLKEPKAAWE-1HFAQQGTPEKFLSLHGGK 177
 QY 306 YFVQVRCNPGIYSGKKAGIWEWSHPTASTP 338
 DB 178 YLVQVRCKP-----DHGYWSAMSPATFIQIP 203

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 AC P40189; Q9UQ41;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, last sequence update)
 DT 25-OCT-2004 (Rel. 45, last annotation update)
 DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (interleukin
 6 signal transducer) (Membrane glycoprotein I30) (gp130) (Oncofostatin M
 receptor) (CDW130) (CD130 antigen).
 DE Name=IL6ST;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Myeloma, and Placenta;
 RX MEDLINE=91084844; PubMed=2261637; DOI=10.1016/0092-8674(90)90411-7;
 RA Hibi M., Murakami M., Saito M., Hirano T., Tega T., Kishimoto T.;
 RT "Molecular cloning and expression of an IL-6 signal transducer,
 gp130."
 RL Cell 63:1149-1157(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Synovium;
 RX MEDLINE=20341529; PubMed=10880057;
 RA Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,
 RA Murakami M., Nakao K.;
 RT "Cloning of novel soluble gp130 and detection of its neutralizing
 RT autoantibodies in rheumatoid arthritis."
 RL J. Clin. Invest. 106:137-144(2000).
 RN [3]
 RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=21269388; PubMed=11098061; DOI=10.1074/jbc.M009979200;
 RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;
 RT "Determination of the disulfide structure and N-glycosylation sites of

[illegible]

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QY 99 IANINGSRORSBDNLVCHARDGSIAGSCLYVGLPPEKPVNISGWSKNMHLTCRWTPGA 158
Db 91 FTDVVLBSVOLTCNIIISFGQIBQNVYGVYMLSGFPDPKPTNLTICIVNEGKNMLCQMDPGR 150
QY 159 HGETFLHTNYSLKXKLMWYQD-NTCEBYHTVGPBHSCHIPKDLALFTPYEIWWEATNRLG 217
Db 151 --ETYLETNYTLKSE--WATEKFPDQSKHGT--SCWVSVMPTYYNIEWWEAENALG 203
QY 218 SARSDVLTLDLIDVYTTDPPPDVHVSRYGLEDQLSVRWVSPFALKDFLQAKYQIRYRV 277
Db 204 KVSSESINFPDVKXKPTPPYNLSVTNSEBLSITLKLWVSSGL--GGLDLKSDIOYRT 261
QY 278 EDSVDMKVY--DDVSNQTSCTRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSMSHPTA 334
Db 262 KDASTWIOVPLEDIMSPTISFTVQDLKFTIEYVRIR---SIKDSGK-GYMSDMSSEAS 316
QY 335 AST--PRSERP 343
Db 317 GTTYEDRPSRP 327

Search completed: February 24, 2005, 03:36:05
Job time : 175 secs

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3	1572.4	75.6	1716	6	AF059293	Homo sapi
4	1572.4	75.6	1740	6	AX205028	Sequence
5	1572.4	75.6	1740	6	AX205042	Sequence
6	1572.4	75.6	1787	6	BD204628	U4 belong
7	1572.4	75.6	1790	6	BD140543	Polypepti
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9	1572.4	75.6	1790	6	AR543953	Sequence
10	1572.4	75.6	1802	9	AY358291	Homo sapi
11	1572.4	75.6	1804	9	AF073515	Homo sapi
12	1572	75.6	1813	6	AR164089	Sequence
13	1570.8	75.6	1650	6	AF178684	Homo sapi
14	1570.8	75.6	1690	6	AF164088	Sequence
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16	1511.6	72.7	1579	6	BD204627	U4 belong
17	1511.6	72.7	1579	6	BD056970	Member of
18	1450.4	69.8	1491	6	CQ726242	Sequence
19	1425	68.5	1498	6	BD221766	Human rec

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25	1219.6	58.7	2162	6	AX364938	Sequence	
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32	1010.2	48.6	1673	6	A70384	Mus muscu	
33	1010.2	48.6	1673	6	BD010515	Sequence	14
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37	1006	48.4	1724	6	AR164000	Member of	
38	972.4	46.8	1218	6	AR139796	Sequence	
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ALIGNMENTS

RESULT 1

LOCUS	A97100	1716 bp	DNA	linear	PAT 26-JAN-2000
DEFINITION	Sequence 24 from Patent WO920755.				
ACCESSION	A97100				
VERSION	A97100.1	GI:6780518			

SOURCE ORGANISM	unidentified unidentified unclassified.
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REFERENCE	AUTHORS
1 (bases 1 to 1716)	Kosco-Vilbois, M. and Gauchat, J.

TITLE NOVEL CYTOKINE RECEPTORS
Patent: WO 9920755-A 24 29-APR-1999;
JOURNAL

Source	Location/Qualifiers	Features
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/organism="unidentified"  
/mol_type="unassigned DNA"  
/db_xref="taxon:32644"
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ORIGIN

Query Match	75.6%	Score 1572.4	DB 6	Length 1716
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Best Local Similarity 99.7%; Pred. NO. 1.8e-288;
Matches 1586; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

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Db 96 GCGCCCCCGGAGCGCCGCCCATGTCCCGCCGGCGCCGGGGGCCCCCGCCGCCCAATCCG 155

550 CGCGCGGCGCGCGCGCTTGCAGCCC---CTGCTGCTGCTCTGCGTCTCGGGGCGCGCG 605

D_b 156 CGCGGCGGGCCGCCGTGGCTGCAGTCTGTGCGATCCTCGGGGGCGCCGC 215

607 GAGCCGGATCAGGAGGCCACACAGCTGTGATCAGTCCCGAGATCCACGGCTTCTCATCG 666

Db 216 GAGCCGGATCAGGAGCCCAACACAGCTGTGATCACTTCCCCAGGATCCACCGCTTCTCATTCG 275

667 GCTCTCCCTGCTGACCACTTGCTCAATGCAAGGAGACCCACAGAGCCACGCCAGG 726

Db 276 GCTCTCCCTGCTGSGCACCTTGCTCAGTGCACGAGACCCACCAAGG 335

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OY	787	CCTCCACCTTGGGCTCTGGCCCTGGCCCAACTCAATGGGTCGAAGCACCGGTCGGGGGACA	846
Db	396	CCTCCACCTTGGGCTCTGGCCCTGGCCCAACTCAATGGGTCGAAGCACCGGTCGGGGGACA	455
OY	847	ACCTGTGTGCGCAAGCCCGTGAACGGCAGACATCCTGGCTGGCTCTGGCTCTAATGTGGCC	906
Db	456	ACCTGTGTGCGCAAGCCCGTGAACGGCAGACATCCTGGCTGGCTCTGGCTCTAATGTGGCC	515
OY	907	TGCCCCCGAGAAAACCCGTCACATCACTAGCTGCTGATCCAAAGACATAGACCTTGACCT	966
Db	516	TGCCCCCGAGAAAACCCGTCACATCACTAGCTGCTGATCCAAAGACATAGACGACTTGACCT	575
OY	967	GCCGTGAGCGCCAGGGGCCCAAGGGGAGACTTTCCTCCACACCACTACTCCCTCAAGT	1026
Db	576	GCCGTGAGCGCCAGGGGCCCAAGGGGAGACTTTCCTCCACACCACTACTCCCTCAAGT	635
OY	1027	ACAGGCTTAGGGGTGATGATGGCCAGGACAACAATGTGAGAGATACACACAGTGGGGCCCC	1086
Db	636	ACAGGCTTAGGGGTGATGATGGCCAGGACAACAATGTGAGAGATACACACAGTGGGGCCCC	695
OY	1087	ACTCTGCGACATCCGCCAAGGACCTGGCTCTTTACGCGCCTATGAATCTGGGTGAGG	1146
Db	696	ACTCTGCGACATCCGCCAAGGACCTGGCTCTTTACGCGCCTATGAATCTGGGTGAGG	755
OY	1147	CCATCCACCGGCTGGGCTCTGCGCGCTCCGATGATACATCAGCTGGATATCTCTGGATG	1206
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Db	816	TGACCAACGAGACCCCGCGCCGACGTCGACGTAAGCCGTCGGGGGCCCTGAGGACCAAC	875
OY	1267	TGAGCGTGCGCTGGGTGTGTGCAACCGCGCTCAAGAGATTTCTCTTCAACCCAAATACC	1326
Db	876	TGAGCGTGCGCTGGGTGTGTGCAACCGCGCTCAAGAGATTTCTCTTCAACCCAAATACC	935
OY	1327	AGATCCGCTACCGAATGAGAGACAATGTGTGACTGGAGAGTGTGTGACGATGTGACACC	1386
Db	936	AGATCCGCTACCGAATGAGAGACAATGTGTGACTGGAGAGTGTGTGACGATGTGACACC	995
OY	1387	AGACTCTCTGCGCGCTGTGGCGCGCTGAACCCCGGACCTGTATCTTGTGAAATGTGGCT	1446
Db	996	AGACTCTCTGCGCGCTGTGGCGCGCTGAACCCCGGACCTGTATCTTGTGAAATGTGGCT	1055
OY	1447	GGAACCCCTTTGGGATCTATGGCTCCAAAGAAAGCCGGATCTGAGGTAGTGAAGCCACC	1506
Db	1056	GGAACCCCTTTGGGATCTATGGCTCCAAAGAAAGCCGGATCTGAGGTAGTGAAGCCACC	1115
OY	1507	CCACAGCCGCTCACTCCCGCAGTGAAGCGCCCGGAGCCCGGGCGCGGGGCGTGCAGAC	1566
Db	1116	CCACAGCCGCTCACTCCCGCAGTGAAGCGCCCGGAGCCCGGGCGCGGGGCGTGCAGAC	1175
OY	1567	CGCGGGGCGGAGAGCGCAGCTGGGGCGGGGTGCGGGGGGAGGCTCAAGGATTTCTCGGACT	1626
Db	1176	CGCGGGGCGGAGAGCGCAGCTGGGGCGGGGTGCGGGGGGAGGCTCAAGGATTTCTCGGACT	1235
OY	1627	GGCTCAAGAGACGCGTACTGCTCCACCTCAGCTTCGCGCTCTACGACAGATGGCGAG	1686
Db	1236	GGCTCAAGAGACGCGTACTGCTCCACCTCAGCTTCGCGCTCTACGACAGATGGCGAG	1295
OY	1687	CCTGATGCAAGATGTGCAACAAGCTCCGACACAGAGCAGAGGGATCTCTGGCTTCGGGCA	1746
Db	1296	CCTGATGCAAGATGTGCAACAAGCTCCGACACAGAGCAGAGGGATCTCTGGCTTCGGGCA	1355
OY	1747	GACGGGGCAACGGGAGAGTCTCGACAGATTAAGCTGTAGGGGCTCAGGCAACCTCTCGTG	1806
Db	1356	GACGGGGCAACGGGAGAGTCTCTCGACAGATTAAGCTGTAGGGGCTCAGGCAACCTCTCGTG	1415
OY	1807	CCACGTGAGACGACAGGCCGAAACCAATCGGGGCCACTCTGTACCTCTCATTTCAAG	1866

Accession	Sequence	Position
Db	CGACGTGAGACGACGAGGCCGAAACCCAACTGGGGCCACTCTGTACCTTCATTACAG	1416
Qy	GCACCTGAGCCACCTCTACGACGAGCTGGGGTGGCCCTTGAGCTTCACACGGCCATTAACAG	1867
Db	GCACCTGAGCCACCTCTACGACGAGGCTGGGGTGGCCCTTGAGCTTCACACGGCCATTAACAG	1476
Qy	CTGTGACTCCACGCTGAGGCCACCTTTGGGTGACCCCGAGTGGTGTGTGTGTGTGTG	1927
Db	CTGTGACTCCACGCTGAGGCCACCTTTGGGTGACCCCGAGTGGTGTGTGTGTGTGTG	1536
Qy	AGGGTGGTGTGAGTGGCTTACAGCCCGCCAGAGGCTGGGGGTGAGAAAGGGAGTATTA	1987
Db	AGGGTGGTGTGAGTGGCTTACAGCCCGCCAGAGGCTGGGGGTGAGAAAGGGAGTATTA	1556
Qy	CTCCCATTAACCTTACGAGGCCCTCCAAAAAGA	2047
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RESULT 2	BD138607	1716 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	BD138607				
DEFINITION	Novel cytokine receptors.				
ACCESSION	BD138607				
VERSION	BD138607.1	GI:23233552			
KEYWORDS	JP 2002508922-A/14.				
SOURCE	unidentified				
ORGANISM	unidentified				
REFERENCE	1 (bases 1 to 1716)				
AUTHORS	Elson,G., Gauchat,J.F. and Vilbois,M.K.				
TITLE	Novel cytokine receptors				
JOURNAL	Patent: JP 2002508922-A 14 26-MAR-2002;				

COMMENT	OS	Unidentified
PN	JP 2002508922-A/14	
PD	26-MAR-2002	
PF	14-OCT-1998 JP 2000517076	
PR	16-OCT-1997 GB 9721961.2	
PI	GREG ELSON, JEAN FRANCOIS GAUCHAT, MARIE KOSCO VILBOIS PC	
C12N15/09	A61K31/7088, A61K38/00, A61K39/395, A61K45/	PC
00, A61K48/00,		
PC	A61P3/04, A61P35/00, A61P37/02, C07K14/715, C07K16/28, C12P21/02//	
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CC	Novel cyclokin receptors	
FM	key	Location/Qualifiers
FT	source	1. .11716
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FEATURES	Location/Qualifiers
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Query Match 75.6%; Score 1572.4; DB 6; Length 1716;

Best Local Similarity 99.7%; Pred. No. 1.8e-288;
 Matches 1586; Conservative 0; Mismatches 1; Indels 3; Gaps 1

[illegible][illegible]

D6 96 GCGCCCCGAGCGTGGCCCAATGCCGCGCCTGCCTGTTCACATCCC

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Db 216 GAGCCGGATCAGAGGCCACACAGCTGTGATCAGTCCCCAGATCCACGCTTCTCATCG 275

QY	667	GCTCCTCCCTCTGGCCACCTGCTCAGTGCAGGAGACCCACACAGAGACCAACCGCCAGG	726
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QY	727	GCTCTACTGACCCCTCAATGAGCGCGCCGCCCTGAGCTCTCCGCTGACTCAAG	786
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QY	907	TGCCCCCAGAGAAACCCGTCAACATCACTGACTGTGTCCAGAACATGAGAGACTTGACT	966
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QY	967	GCCGCTGACGCGCAGGGGCCACAGGGGAGACTTCTTCACACCAACTTCCTCAAGT	1026
Db	576	GCCGCTGACGCGCAGGGGCCACAGGGGAGACTTCTTCACACCAACTTCCTCAAGT	635
QY	1027	ACAAGCTTAAGGTGATGATGCCAGGACAAACAATGAGAGATGACACACATGGGGCCCC	1086
Db	636	ACAAGCTTAAGGTGATGATGCCAGGACAAACAATGAGAGATGACACACATGGGGCCCC	695
QY	1087	ACTCTGCGCACATCCCCAAGGACCTGGCTCTTTACCCGCTATGAGATCTGGGTGAGG	1146
Db	696	ACTCTGCGCACATCCCCAAGGACCTGGCTCTTTACCCGCTATGAGATCTGGGTGAGG	755
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Db	756	CCACCAACCGCCTGGGCTCTGCGCGCTTCGATGATCTACGCTGAGATTCCTGATGTGG	815
QY	1207	TGACCAAGGACCCCCCGGCCGACGTGACAGTGAAGCGCGGTGGGGGCTTGAAGACCAAG	1266
Db	816	TGACCAAGGACCCCCCGGCCGACGTGACAGTGAAGCGCGGTGGGGGCTTGAAGACCAAG	875
QY	1267	TGAGCGTACGCTGGGTGTGCGCACCGGCCCTCAAGAGATTTCTCTTTCAAGCCAAATAC	1326
Db	876	TGAGCGTACGCTGGGTGTGCGCACCGGCCCTCAAGAGATTTCTCTTTCAAGCCAAATAC	935
QY	1327	AGATCCGTTACCGAGTGAAGGACAGTGTGACTGGAAGTGGTGAACGATGTGACACCC	1386
Db	936	AGATCCGTTACCGAGTGAAGGACAGTGTGACTGGAAGTGGTGAACGATGTGACACCC	995
QY	1387	AGACTCTCTGCGCGCTGGCGCGGCTTGAAACCGGGACCGTGTACTTGTGCAATGGCT	1446
Db	996	AGACTCTCTGCGCGCTGGCGCGGCTTGAAACCGGGACCGTGTACTTGTGCAATGGCT	1055
QY	1447	GCAACCCCTTTGGCATCTATGGCTCCAGAAAGCCGGATCTGAGGTGAGTGAAGCCAC	1506
Db	1056	GCAACCCCTTTGGCATCTATGGCTCCAGAAAGCCGGATCTGAGGTGAGTGAAGCCAC	1115
QY	1507	CCACAGCGGCTTCCACTCCCGCCAGTGAAGCGCCCGGGCCCGGGCCGCGGGCGTTCGAA	1566
Db	1116	CCACAGCGGCTTCCACTCCCGCCAGTGAAGCGCCCGGGCCCGGGCCGCGGGCGTTCGAA	1175
QY	1567	CGCGGGGCGGAGAGCGGAGCTTCGGGGCGGGTCCGAGCTCAAGCAGATTCCTGGGCT	1626
Db	1235	CGCGGGGCGGAGAGCGGAGCTTCGGGGCGGGTCCGAGCTCAAGCAGATTCCTGGGCT	1286
QY	1627	GGCTCAAGAGACCGGTACTGCTCAACCTCAGCTTCGGCTCAAGACCAAGTGGCAG	1686
Db	1286	GGCTCAAGAGACCGGTACTGCTCAACCTCAGCTTCGGCTCAAGACCAAGTGGCAG	1345
QY	1687	CCTGATCAGAGATGCGACAAAGACCCGCAACAGAGAGAGATCTGCGCTTCGGGCA	1746
Db	1355	CCTGATCAGAGATGCGACAAAGACCCGCAACAGAGAGAGATCTGCGCTTCGGGCA	1405
QY	1747	GACGGGGACGCGGAGAGGTCTCTGCCAATATAGGAGGCTTCAGGCCACCTTCCTG	1806

Df	1356	GACGGGAGCAGCGAGAAGTCTGTCCAGATTAAGCTGAAGGGGCTCAAGGCCACTCCCTG	1415
OY	1807	CCACGTGAGACGCAGAGGCCGAACCCAACTGGGGGCACTCTGTACCTCTCACTTCAGG	1866
Df	1416	CCAGGTGAGACGCAGAGGCCGAACCCAACTGGGGGCACTCTGTACCTCTCACTTCAGG	1475
OY	1867	GCACCTTAGACCACTCTAGACAGAGGCTGGGGTGCCCCCTAGAGCTCAAACGGCCATTACAG	1926
Df	1476	GCACCTTAGACCACTCTAGACAGAGGCTGGGGTGCCCCCTAGAGCTCAAACGGCCATTACAG	1535
OY	1927	CTCTGACTCCACACGTGAGGCCAAGCTTTGGGTGACACCACAGTGGGTGTGTGTGTGTGTG	1986
Df	1536	CTCTGACTCCACACGTGAGGCCAAGCTTTGGGTGACACCACAGTGGGTGTGTGTGTGTGTG	1595
OY	1987	AGGGTTGGTTGAGTTGGCTTAGAACCCCTGCCAGGGCTGGGGGTGAGAAAGGGAGTCAATTA	2046
Df	1596	AGGGTTGGTTGAGTTGGCTTAGAACCCCTGCCAGGGCTGGGGGTGAGAAAGGGAGTCAATTA	1655
OY	2047	CTCCCCATTACCTTAGGGGCCCCCTCCAAAAGA	2076
Df	1656	CTCCCCATTACCTTAGGGGCCCCCTCCAAAAGA	1685

RESULT 3
AF059293

LOCUS AF059293

DEFINITION Homo sapiens cytokine-like factor-1 precursor (CDF-1) mRNA,
complete cds.

ACCESSION AF059293

VERSION AF059293.1 GI:3372626

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE

REFERENCE

AUTHORS Elson,G.C., Graber,P., Losberger,C., Herren,S., Gretenier,D.,
Menoud,L.N., Wells,T.N.C., Kosco-Villbois,M.H. and Gauchat,J.F.
Cytokine-like factor-1, a novel soluble protein, shares homology
with members of the cytokine type I receptor family

JOURNAL J. Immunol. 161 (3), 1371-1379 (1998)

MEDLINE 98349389

PUBMED 9686600

REFERENCE

AUTHORS Elson,G.C.A., Graber,P., Losberger,P., Herren,S., Gretenier,D.,
Menoud,L.N., Wells,T.N.C., Kosco-Villbois,M.H. and Gauchat,J.F.
Direct Submission

TITLE Submitted (14-APR-1998) Dept. of Immunology, Seroo Pharmaceutical
Research Institute, 14, Chemin des Aulx, Plan-Ies-Ouates, CH 1228,
Switzerland

FEATURES

SOURCE location/Qualifiers

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similar to the sequence presented in GenBank Accession
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gene

CDS

FEATURES	PIERRE	FABRE	MEDICAMENT (PR)
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	GETFLHNYSLKYRLRMWGMDNCEBHTVPHSGHLPKDALPLPYEIVWEANRNG		
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	RVEDSVDMKVVDVSNQTSRCLAGIKPETVYFVQVRCPPEIYYSKAKGIMSEKSHPT		
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ORIGIN

Query Match	75.6%;	Score 1572.4;	DB 6;	Length 1740;
Best Local Similarity	99.7%;	Pred. No. 1.8e-286;		
Matches 1886;	Conservative	0;	Mismatches 1;	Indels 3;
				Gaps 1;

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QY	1267	TGAGCGTGGCGTGGGTGTGCGCAACCGCGCCTCAAGATTTCTCTTTCAAGCCAAATACC	1326
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QY	1327	AGATCCGCTTACCGAGTGTGAAGAAACAGTGTGACCTGGAAGTGTGTGGAAGATGTGACAAC	1386
Db	948	AGATCCGCTTACCGAGTGTGAAGAAACAGTGTGACCTGGAAGTGTGTGGAAGATGTGACAAC	1007
QY	1387	AGACCTTCCTGCGCGCTTGCGCGCGCTTGAACCCCGCACCGTGTACTTTGTGCAATGTGCGCT	1446
Db	1008	AGACCTTCCTGCGCGCTTGCGCGCGCTTGAACCCCGCACCGTGTACTTTGTGCAATGTGCGCT	1067
QY	1447	GCAACCCCTTTTGGCATCTATGTGCTTCAAGAAAGCCGGGATCTTGGAGTGTGTGAGCCAAC	1506
Db	1068	GCAACCCCTTTTGGCATCTATGTGCTTCAAGAAAGCCGGGATCTTGGAGTGTGTGAGCCAAC	1127
QY	1507	CCAACGCGCGCTCCACTCCCGCGAGTAGCGGCCCGGGCGGGGCGGGGCGTGCACAC	1566
Db	1128	CCAACGCGCGCTCCACTCCCGCGAGTAGCGGCCCGGGCGGGGCGGGGCGTGCACAC	1187
QY	1567	CGCGGGCGGAGAGACCGAGCTCGGGGCGGGGTGCGGCGCGAGCTCAGCAATTCTTGCGCT	1626
Db	1188	CGCGGGCGGAGAGACCGAGCTCGGGGCGGGGTGCGGCGCGAGCTCAGCAATTCTTGCGCT	1247
QY	1627	GGCTCAAGAAAGCAAGCGCTACTGTCTCAACCTCAAGCTTCGCGCTCTAGACAAGTGTGGGAG	1686
Db	1248	GGCTCAAGAAAGCAAGCGCTACTGTCTCAACCTCAAGCTTCGCGCTCTAGACAAGTGTGGGAG	1307
QY	1687	CTTGAGTGTCAAGATGTGCAACAAGACCCGCAACCAAGACGAAGGAGTCTTGCCCTGCGACA	1746
Db	1308	CTTGAGTGTCAAGATGTGCAACAAGACCCGCAACCAAGACGAAGGAGTCTTGCCCTGCGACA	1367
QY	1747	GACGGGGCGAGCGAGAGTGTCTGCGCAGATTAAGTGTAGGGGCTCAAGCCACCTCCCTG	1806
Db	1368	GACGGGGCGAGCGAGAGTGTCTGCGCAGATTAAGTGTAGGGGCTCAAGCCACCTCCCTG	1427
QY	1807	CCAGCTGAGAGCGAGAGGCGCAACCCAAACTGCGGCGCACTCTGTACCTCTCATCTTCAGG	1866
Db	1428	CCAAGTGTGAAGCGAGAGGCGCAACCCAAACTGCGGCGCACTCTGTACCTCTCATCTTCAGG	1487
QY	1867	GCACCTTAGACCACTCTAGACGAGGCTGGGGTGCCCTCTGAGCTTCAACGCGCATTAACG	1928
Db	1488	GCACCTTAGACCACTCTAGACGAGGCTGGGGTGCCCTCTGAGCTTCAACGCGCATTAACG	1547
QY	1927	CTTGAAGTCCCAAGTGAAGCCACTTTTGGGTGACCCCAAGTGGGTGTGTGTGTGTG	1986
Db	1548	CTTGAAGTCCCAAGTGAAGCCACTTTTGGGTGACCCCAAGTGGGTGTGTGTGTGTGTG	1607
QY	1987	AGGGTGTGTGAGTGTGCTTAGAACCTCTGCCAGGCGTGTGGGGTGAAGAGGGAGTCATTA	2046
Db	1608	AGGGTGTGTGAGTGTGCTTAGAACCTCTGCCAGGCGTGTGGGGTGAAGAGGGAGTCATTA	1667
QY	2047	CTCCCCATTACTTAGGGGCGCTCCAAAAGA 2076	
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RESULT 6	BD204628	BD204628	1787 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD204628					
DEFINITION	U4 belonging to hematopoietin receptor superfamily.					
ACCESSION	BD204628					
VERSION	BD204628.1	GI:33014398				
KEYWORDS	JP 2002511268-A/5.					
SOURCE	unidentified					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 1787)					
AUTHORS	Donaldson,D., Collins,M., Whitters,M. and Neben,T.					

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Dd	576	GCCGCTGGACGCCAGGGGGCCCACGGGGAGACTTTCCTCCACAACAATACTCCTCCAGT	635
OY	1027	ACAAGCTTAGGTGGATATGGCCAAGAACAACATGTGAAGAGTACCAACAAGTGGGGCCCC	1086
Dd	636	ACAAGCTTAGGTGGATATGGCCAAGAACAACATGTGAAGAGTACCAACAAGTGGGGCCCC	695
OY	1087	ACTCTTGCCACATCCCCAAGGACTGTGCCTCTCTTTACGCCCTATGAGATCTGGGTGAGG	1146
Dd	696	ACTCTTGCCACATCCCCAAGGACTGTGCCTCTCTTTACGCCCTATGAGATCTGGGTGAGG	755
OY	1147	CCACCACCCGCTGGGGCTGTGCCCGGCTCCCATGTACTCACGCTGGGAATATCCTGGATGTGG	1206
Dd	756	CCACCACCCGCTGGGGCTGTGCCCGGCTCCCATGTACTCACGCTGGGAATATCCTGGATGTGG	815
OY	1207	TGACCACGSAACCCCOCGCCGACGTGACAGTGACCGCGCTCGGGGGCTGTGAGGACGACG	1266
Dd	816	TGACCACGSAACCCCOCGCCGACGTGACAGTGACCGCGCTCGGGGGCTGTGAGGACGACG	875
OY	1267	TGAGCGTGCGCTGGGTGTCCGCAACCCGCGCTCAAAGATTCTCTTTCAAGCCAAATATCC	1326
Dd	876	TGAGCGTGCGCTGGGTGTCCGCAACCCGCGCTCAAAGATTCTCTTTCAAGCCAAATATCC	935
OY	1327	AGATCCGCTAACGAGTGGAGGACAGTGTGGACGTGAAGAGTGGTGAACGATGTGACAAC	1386
Dd	936	AGATCCGCTAACGAGTGGAGGACAGTGTGGACGTGAAGAGTGGTGAACGATGTGACAAC	995
OY	1387	AGACCTCTCTGCGCTGTGGCCTGGACCTGAAACCCCGGACCGTGTATCTTGTGTCAATGTGCT	1446
Dd	996	AGACCTCTCTGCGCTGTGGCCTGGACCTGAAACCCCGGACCGTGTATCTTGTGTCAATGTGCT	1055
OY	1447	GCAACCCCTTTGGGATCTATGTGCTTCAAGAAAGCCGGGAATCTGGAGTGAAGTGGACCAAC	1506
Dd	1056	GCAACCCCTTTGGGATCTATGTGCTTCAAGAAAGCCGGATCTGGAAGTGAAGTGGACCAAC	1115
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Dd	1116	CCACAGCCGCGCTCACTCCCGCAGTGAAGCGCCCGGCGCGGGGGCGGGGCGTGGCGAAC	1175
OY	1567	CGCGGGCGGAGAGCCGAGCTCGGGGCGGTGTGCGGCGAGCTCAAGCAATTCTTGCGCT	1626
Dd	1176	CGCGGGCGGAGAGCCGAGCTCGGGGCGGTGTGCGGCGAGCTCAAGCAATTCTTGCGCT	1235
OY	1627	GGCTCAAGAAACAAGCGCTATCTGTCTTCCAAACCTCACTTCGCGCTTAAGACCAAGTGGCGAG	1686
Dd	1236	GGCTCAAGAAACAAGCGCTATCTGTCTTCCAAACCTCACTTCGCGCTTAAGACCAAGTGGCGAG	1295
OY	1687	CCTGGATGCAAAATCGCACAAAGACCCGCAACAGACAGAGGGATCTGCTCGCGGCA	1746
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OY	1747	GACGGGGCAGCGGAGAGGTCTTCCAGATTAAGCTTATAGGGGCTCAGGCCACCTCCCTG	1806
Dd	1356	GACGGGGCAGCGGAGAGGTCTTCCAGATTAAGCTTATAGGGGCTCAGGCCACCTCCCTG	1415
OY	1807	CCAGTGGAGACGAGAGGGCCGAACCCAAATCTGGGGCAACCTGTATCCCTCATTTAGG	1866
Dd	1416	CCAGTGGAGACGAGAGGGCCGAACCCAAATCTGGGGCAACCTGTATCCCTCATTTAGG	1475
OY	1867	GCACCTGAGCACCCCTCAGCAGAGACTGGGGTGGCCCTGAGCTTCAACGCGCCATAACAG	1926
Dd	1476	GCACCTGAGCACCCCTCAGCAGAGACTGGGGTGGCCCTGAGCTTCAACGCGCCATAACAG	1535
OY	1927	CTCTGACTCCACGATGAGGCCACTTTTGGGTGACCCCAAGTGGGTGTGTGTGTGTGTG	1986
Dd	1536	CTCTGACTCCACGATGAGGCCACTTTTGGGTGACCCCAAGTGGGTGTGTGTGTGTGTG	1595
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OY		1867	GCACCTGAGCCACCCTCAGAGAGACTGGGTGGGCCCTGAGCTCAACCGCATAAACG	1928
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OY		1927	CTTGACTCCCACTGAGGCCACCTTTGGGTGACACCCAGTAGTGTGTGTGTGTG	1988
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DEFINITION	Sequence 1 from patent US 6271343.			
ACCESSION	AR164088			
VERSION	AR164088.1	GI:16235032		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 1690)			
TITLE	Lok,S., Presnell,S.R., Jelineberg,A.C., Gilbert,T., Whitmore,T.E., Foester,D.C., Adams,R.L. and Lohner,J.M. Mammalian cytokine-like receptor 5 Patent: US 6271343-A 1 07-MUG-2001;			
JOURNAL	Location/Qualifiers			
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OY		550	GCGGCGGCGCCGCGCGCGCTTGTCTGCC--CTGCTGCTGCTTGTGCGTCTTGCGGCGCGCG	606
Db		89	GCGGCGGCGCGCGCGCGCTTGTCTGCC--CTGCTGCTGCTTGTGCGTCTTGCGGCGCGCG	148
OY		607	GAGCGCGGATCGAGAGCCCAACAGCTGTGATCAAGTCCCAAGATCCCAAGCTTCTCAATCG	666
Db		149	GAGCGCGGATCGAGAGCCCAACAGCTGTGATCAAGTCCCAAGATCCCAAGCTTCTCAATCG	208
OY		667	GCTCCTCCTGCTGCGCACTTCTCAGTGAAGAGAGACCAACAAGAGCCACCGCGAGG	726
Db		209	GCTCCTCCTGCTGCGCACTTCTCAGTGAAGAGAGACCAACAAGAGCCACCGCGAGG	268
OY		727	GCTTCTACTGGAACCTCAATGAGCGCGCGCTGCGCCCTGAGCTCTCCCTGTACTCAAAG	786
Db		269	GCTTCTACTGGAACCTCAATGAGCGCGCGCTGCGCCCTGAGCTCTCCCTGTACTCAAAG	328
OY		787	CCTCAACTTGGCTGTGCGCCGCGCAACTCAATGGGTCCAGAGCAGGAGTCCGAGGAGCA	846
Db		329	CCTCAACTTGGCTGTGCGCCCTGAGCAACTCAATGGGTCCAGAGCAGGAGTCCGAGGAGCA	388
OY		847	ACCTGTGTGCCACGCGCCGTGAAGCGGACAGATCTTGCTGTGCTCTCTATGTGTGCC	906
Db		389	ACCTGTGTGCCACGCGCCGTGAAGCGGACAGATCTTGCTGTGCTCTCTATGTGTGCC	448
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Db	449	GGCCCCCAGAGAAA	CCCGTCAACATCAGCTGCTGTGCTCCAAACATCATGAAGGACTTGAACCT	508		
.QY	967	GCCCGTGGACGCC	CAGGGGGCCCA	CGGGGAGACCTTCTCTCACAACA	CTACTCTCCTCAAGT	1026
Db	509	GCCCGTGGACGCC	CAGGGGGCCCA	CGGGGAGACCTTCTCTCACAACA	CTACTCTCCTCAAGT	568
QY	1027	ACAAGCTTAAGGTG	GATATGAGCCAGGACA	CAACATGTGAGGAGTATCAACA	CAGTGGGGCCCC	1086
Db	569	ACAAGCTTAAGGTG	ATATGAGCCAGGACA	CAACATGTGAGGAGTATCAACA	CAGTGGGGCCCC	628
QY	1087	ACTCTGCGCAATCC	CCCAAGGACCTGGCTCTTTACG	CCCTATGAGATCTGGGTGAGG		1146
Db	629	ACTCTGCGCAATCC	CCCAAGGACCTGGCTCTTTAG	CCCTATGAGATCTGGGTGAGG		688
QY	1147	CCACCAACCGCT	TGGGCTCTG	CCCGCTCCGATGTATCA	CGCTGATATCTTGAATGG	1206
Db	689	CCACCAACCGCT	TGGGCTCTG	CCCGCTCCGATGTATCA	CGCTGATATCTTGAATGG	748
QY	1207	TGACCAAGGACCC	CCCCCGCGAGCGTGA	CGAGACCGCGTGGGGGGCTG	AGGACAAGC	1266
Db	749	TGACCAAGGACCC	CCCCCGCGAGCGTGA	CGAGACCGCGTGGGGGGCTG	AGGACAAGC	808
QY	1267	TGAGCGTGCCTG	GGGTGTGCGCACCCG	CCCTCAAGATTTCTTTCAAG	CCAAATATC	1326
Db	809	TGAGCGTGCCTG	GGGTGTGCGCACCCG	CCCTCAAGATTTCTTTCAAG	CCAAATATC	868
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QY	1387	AGACCTCTGCGG	CTGTGGCGGCTTGAA	CCCCGCAACCGTATCTTGTGTGA	AAATGGCT	1446
Db	929	AGACCTCTGCGG	CTGTGGCGGCTTGAA	CCCCGCAACCGTATCTTGTGTGA	AAATGGCT	988
QY	1447	GCAACCCCTTTGG	ATCTATGTGCTCCAAAGAA	AGCCGGATCTGAGTGTGAGGACCA	CC	1506
Db	989	GCAACCCCTTTGG	ATCTATGTGCTCCAAAGAA	AGCCGGATCTGAGTGTGAGGACCA	CC	1048
QY	1507	CCACAGCGCGCT	CACTCCCGCAGTGA	CGCCCCGGGCGCGGGCGGTG	CGAAC	1566
Db	1049	CCACAGCGCGCT	CACTCCCGCAGTGA	CGCCCCGGGCGCGGGCGGTG	CGAAC	1108
QY	1567	CGCGGGGCGAG	AGACCCGAGCTCGGGGCGG	GTGCGGCGCAGCTCA	AGCATTTCTTGGGCT	1626
Db	1109	CGCGGGGCGAG	AGACCCGAGCTCGGGGCGG	GTGCGGCGCAGCTCA	AGCATTTCTTGGGCT	1168
QY	1627	GGCTCAAGAA	CAAGCGGATCTGTCCAA	CCCTCAGCTTCCGCTCTA	GACAAGGAGG	1686
Db	1169	GGCTCAAGAA	CAAGCGGATCTGTCCAA	CCCTCAGCTTCCGCTCTA	GACAAGGAGG	1228
QY	1687	CCTGGATGCA	AAATGCGACAAAGAC	CCCGCAACGAGGAGATCTG	CCCTCGGACA	1746
Db	1229	CCTGGATGCA	AAATGCGACAAAGAC	CCCGCAACGAGGAGATCTG	CCCTCGGACA	1288
QY	1747	GACGGGCGAC	GGCGAGAGTCTGTCCAG	ATATGATGAGGAGCTC	AGGCCACCTTCCCTG	1806
Db	1289	GACGGGCGAC	GGCGAGAGTCTGTCCAG	ATATGATGAGGAGCTC	AGGCCACCTTCCCTG	1348
QY	1807	CCAGTGGAGAG	CGAGAGGCGGAACCCAA	CTGGGGGCACTCTGTATCC	CTCACTTCAAG	1866
Db	1349	CCAGTGGAGAG	CGAGAGGCGGAACCCAA	CTGGGGGCACTCTGTATCC	CTCACTTCAAG	1408
QY	1867	GCACCTGAG	CAACCTTCAAGAGAGCT	GGGGTGCCCTGAGCT	CAACGCGCATTAACAG	1926
Db	1409	GCACCTGAG	CAACCTTCAAGAGAGCT	GGGGTGCCCTGAGCT	CAACGCGCATTAACAG	1468
QY	1927	CTCTGACTCC	CACTGAAGGCCACTTTGG	TGCAACCCAGTGGGTGTGTGTGTGTG		1986
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QY	1987	AGGGTGGTGA	GTGTGCTATGAACCCCTG	CGAGGCGTGGGGGTGAGAAAGGGAGTCA	TTA	2046
Db	1529	AGGGTGGTGA	GTGTGCTATGAACCCCTG	CGAGGCGTGGGGGTGAGAAAGGGAGTCA	TTA	1588

Db	Accession	Version	Keywords	Source	Organism	Reference	Authors
RESULT 15	BC044634						
LOCUS	BC044634						
DEFINITION	Homo sapiens cytokine receptor-like factor 1, mRNA (cDNA clone MGC:52126 IMAGE:5926400), complete cds.						
ACCESSION	BC044634						
VERSION	BC044634.1						
KEYWORDS	MGC:						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE	Eumalazia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
AUTHORS	Klausner R.D., Collins F.S., Wagner L.H., Derg J.G., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Brat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stjepanovic M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E., Brownstein M.J., Udell T.B., Toshitsuki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.U., Bosak S.A., McEwan P.J., McEwan R.C., Hale S., Garcia A.M., Gay L.J., Huliyil S.W., Villalon D.C., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettleman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimmer J., Schmitt J., Myers R.M., Butcherfield V.S., Krzywnicki M.I., Skalska U., Smalls D.E., Scheraga A., Schein J.E., Jones S.J., and Marra M.A.						
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences						
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.						
PUBMED	12477932						
REFERENCE	2 (bases 1 to 1744)						
AUTHORS	Straussberg R.						
TITLE	Direct Submission						
JOURNAL	Submitted (17-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA						
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov						
COMMENT	Contact: MGC help desk Email: gcgaps-remail.nih.gov Tissue Procurement: Lou Staudt CDNA Library Preparation: Rubin Laboratory CDNA library Arrayed by: The I.M.A.G.E. Consortium (ILNLT) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@nih.gov						
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLT at: http://image.llnl.gov Series: ILNLT Plate: 44 Row: O Column: 22. Location/Qualifiers 1..1744						

[illegible]

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QY 1147 CCACCAACCGCTTGGCTTGCCTGCGCTCCGATGTACTACGCTGATATCTGTGATGTG 1206
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mis Page Blank (uspto)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2005, 07:35:16 / Search time 1045 Seconds
(without alignments)
11777.170 Million cell updates/sec

Title: US-09-037-657-43

Perfect score: 2079

Sequence: 1 gcgcattctgtgttccaat.....aggcccccctcaaatgctc 2079

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

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- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
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- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2079	100.0	2079	4 AAD04199	Aad04199 Murine ha
2	1572.4	75.6	1716	2 AAX25489	Aax25489 Human typ
3	1572.4	75.6	1716	6 ABQ88149	Abq88149 Human ost
4	1572.4	75.6	1716	8 ABX14013	Abx14013 Human cyt
5	1572.4	75.6	1716	13 ADR25220	Adr25220 Breast ca
6	1572.4	75.6	1740	4 AAH74486	Aah74486 Nucleotid
7	1572.4	75.6	1787	2 AAX90754	Aax90754 Human U4
8	1572.4	75.6	1789	2 AAX80050	Aax80050 Human PRO
9	1572.4	75.6	1789	10 ADR27451	Adh27451 Human cdn
10	1572.4	75.6	1790	2 AAX87256	Aax87256 cDNA clon
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13	1572.4	75.6	1790	8 ABX78444	Abx78444 DNA encod
14	1572.4	75.6	1790	8 ABX77078	Abx77078 cDNA sequ
15	1572.4	75.6	1790	8 ABX75909	Abx75909 Human cdn
16	1572.4	75.6	1790	8 ABX89620	Abx89620 cDNA enco
17	1572.4	75.6	1790	8 ABX34106	Abx34106 cDNA enco
18	1572.4	75.6	1790	9 ACA04326	Aca04326 Human PRO
19	1572.4	75.6	1790	10 ADC52787	Adc52787 Human cdn
20	1572.4	75.6	1790	10 ADC55545	Adc55545 Human cdn

ALIGNMENTS

21	1572.4	75.6	1790	10 ADC25666	Adc25666 Human CDN
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23	1572.4	75.6	1790	10 ABX89453	Abx89453 Human PRO
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25	1572.4	75.6	1790	12 ADG63443	Adg63443 Human CDN
26	1572.4	75.6	1790	12 ADH43172	Adh43172 Human CDN
27	1572.4	75.6	1790	12 ADN00410	Adn00410 Human CDN
28	1572.4	75.6	1802	3 AAA46902	Aaa46902 cDNA enco
29	1572.4	75.6	1804	6 ABQ88147	Abq88147 Human ost
30	1572.4	75.6	1804	10 ADL13624	Adl13624 Osteoarth
31	1572.4	75.6	1804	12 ADN04231	Adn04231 Antipsoit
32	1572.4	75.6	1804	12 ADQ18850	Adq18850 Human sof
33	1572.4	75.6	2154	12 ADQ23242	Adq23242 Human sof
34	1572	75.6	1813	5 AAV70895	Aav70895 cDNA enco
35	1570.8	75.6	1650	6 ABQ88148	Abq88148 Human ost
36	1570.8	75.6	1690	2 AAV70894	Aav70894 cDNA enco
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40	1433.8	69.0	1882	10 ADF71799	Adf71799 cDNA for
41	1425	68.5	1458	3 AA234614	Aa234614 Human rec
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RESULT 1

AAAD04199	standard; DNA; 2079 BP.
ID	AAAD04199
XX	AAAD04199;
AC	AAAD04199;
XX	AAAD04199;
DT	09-SEP-2004 (revised)
DT	02-JUL-2001 (first entry)
XX	02-JUL-2001 (first entry)
DE	Murine haemopoietin receptor, NR6 DNA.
XX	
KM	Murine; biologically active complex; haemopoietin receptor; NR6;
KW	cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;
KX	differentiation; cell survival; neutrophilic activity; ds.
XX	
OS	Mus sp.
OS	Unidentified.
XX	
FT	Key
FT	Location/Qualifiers
FT	CDS
FT	/*tag= a
FT	/product= "Murine haemopoietin receptor, NR6 protein"
XX	
PN	W0200127157-A1.
XX	
PD	19-APR-2001.
XX	
PF	06-OCT-2000; 2000WO-AU001216.
XX	
PR	08-OCT-1999; 99AU-00003327.
XX	
PR	12-MAY-2000; 2000AU-00007489.
XX	
XX	(AMRA-) AMRAD OPERATIONS PTY LTD.
PA	
XX	
PI	Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;
PI	Nakata Y, Hasegawa M;
XX	
DR	WPI; 2001-281978/29.
XX	
DR	P-PSDB; AAE00826.
XX	
PT	New biologically active complex comprising NR6 and cardiotrophin-like-
PT	cytokine, for facilitating proliferation, differentiation and/or survival
PT	of a cell.

XX Claim 22; Page 102-106; 123bp; English.

CC The present invention relates to a biologically active complex comprising
XX a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC). The
CC complex is useful in the manufacture of a medicament for the treatment
CC and/or prophylaxis of a subject, as it is involved in facilitating
CC proliferation, differentiation and/or survival of a cell. The complex or
CC its components have neurotrophic activity. The present sequence is murine
CC haemopoietin receptor, NR6 DNA

CC Revised record issued on 09-SEP-2004 : Correction to Organism field
CC
CC Sequence 2079 BP; 412 A; 667 C; 602 G; 398 T; 0 U; 0 Other;

Query Match 100.0%; Score 2079; DB 4; Length 2079;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2079; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 421 AGGTTCAATGCTCAAGGGGCAACTCTGTGGGTTAGGATTTAGAGCTTCTGCT 480
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DB 1441 TGGCTGCAACCCCTTGGCATCTATGCTCCAAAGAACCGGATCTGAGTGAATGA 1500
QY 1501 GGCACCCCAAGCCGCTTCACTCCCGGAGTGAAGCGCGCGCGCGCGCGCGCGCGCG 1560
DB 1501 GGCACCCCAAGCCGCTTCACTCCCGGAGTGAAGCGCGCGCGCGCGCGCGCGCGCG 1560
QY 1561 GCGAACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1620
DB 1561 GCGAACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1620
QY 1621 TGGGCTGAGTCAAGAGACGCGTACTGCTCCAACTCAAGTCTTCCGCTCTTACGACAG 1680
DB 1621 TGGGCTGAGTCAAGAGACGCGTACTGCTCCAACTCAAGTCTTCCGCTCTTACGACAG 1680
QY 1681 GGCAGGCTGATGACAGAAATGCGACACAGACCCGAAACAGAGACGAGGAGATCTGCC 1740
DB 1681 GGCAGGCTGATGACAGAAATGCGACACAGACCCGAAACAGAGACGAGGAGATCTGCC 1740
QY 1741 CGGAGAGACGAGGAGACGCGGAGAGGCTGCGCAATGAGCTGTAGGGGCTAGGGCAACC 1800
DB 1741 CGGAGAGACGAGGAGACGCGGAGAGGCTGCGCAATGAGCTGTAGGGGCTAGGGCAACC 1800
QY 1801 TCCCTGCACTGTGAGACGCGAGGCGCGCAACCAATGAGGCGCACTTGTATCCCTCAC 1860
DB 1801 TCCCTGCACTGTGAGACGCGAGGCGCGCAACCAATGAGGCGCACTTGTATCCCTCAC 1860
QY 1861 TTCAAGGGCACTGAGCCACTTCAAGAGAGGCTGAGGCTGAGGCTTCAAGCGCGCA 1920
DB 1861 TTCAAGGGCACTGAGCCACTTCAAGAGAGGCTGAGGCTGAGGCTTCAAGCGCGCA 1920
```


Oy		1921	TAAcAGCCTCTGATCTCCCAcGtGAGGGCAcCTTTGGGTgCACCCAGTGGGTGTGTGTG	1980
Dd		1921	TAAcAGCCTCTGATCTCCCAcGtGAGGGCAcCTTTGGGTgCACCCAGTGGGTGTGTGTG	1980
Oy		1981	TGTGTGAAGGGTTGGTTGAGATTGCCCTAGAACCCTTCGCACAGGCTGGGGGTGAGAAAGGGAG	2040
Dd		1981	TGTGTGAAGGGTTGGTTGAGATTGCCCTAGAACCCTTCGCACAGGCTGGGGGTGAGAAAGGGAG	2040
Oy		2041	TCATTACTCCCCATTACCTTAGGGCCCCCTTCCAAAGATCC	2079
Dd		2041	TCATTACTCCCCATTACCTTAGGGCCCCCTTCCAAAGATCC	2079
<hr/>				
RESULT 2				
ID	AAX25489	AAX25489 standard; cDNA, 1716 BP.		
XX	AAX25489;			
DT	02-AUG-1999	(first entry)		
DE	Human type I cytokine receptor GBRI-ILR cDNA.			
XX				
KW	GBRI-ILR; hGBR-ILR; cytokine receptor; human; cancer; obesity;			
KW	inflammation; septic shock; AIDS; embryo development; lung infection;			
KW	cytostatic; anorectic; immunosuppressive; antibacterial; antiviral;			
KW	antiinflammatory; therapy; ss.			
OS	Homo sapiens.			
FN				
FT	Key	Location/Qualifiers		
FT	CDS	119..1387		
FT		/+tag= a		
FT	sig_peptide	119..229		
FT		/+tag= b		
FT	mat_peptide	230..1384		
FT		/+tag= c		
XX				
PN	WO9920755-A2.			
PD	29-APR-1999.			
XX				
PF	14-OCT-1998;	98WO-EP006497.		
XX				
PR	16-OCT-1997;	97GB-00021961.		
PA	(GLAX) GLAXO GROUP LTD.			
PI	Elson G, Gauchat J, Kosco-Vilbois M,			
DR	WP1: 1999-288305/24.			
XX	P-PsDB; AAY05782.			
PT	Novel human or mouse type I cytokine receptors hGBRI-ILR or mGBRI-ILR,			
PS	useful for treating e.g. cancer, immune disorders, obesity and AIDS.			
PS	Claim 23; Fig 3; 41pp; English.			

This is the nucleotide sequence of a cDNA clone encoding a novel type I cytokine receptor (see AAY05782) that has been termed human GBRI-ILR as it is believed to be an interleukin receptor, or at least a substantial part of such a receptor. To clone the cDNA, a 310 bp PCR product was amplified from human lung cDNA using primers designed from human ESTs that had been identified using the WEXMS motif of the mouse IL-13 receptor alpha 1 as query, and used as a probe to screen a human placental cDNA library. The GBRI-ILR receptor has also been identified in mice (see AAY05783), and the high degree of conservation of amino acids between the human and murine polypeptides indicates that this receptor is functionally important. GBRI-ILR nucleic acids are used for the recombinant production of GBRI-ILR polypeptides, in antisense therapy and as probes and primers. GBRI-ILR polypeptides, nucleic acids, agonists, antagonists and antibodies can be used to treat e.g. cancer, immune

[illegible]

YY	1447	GCAACCCCTTTGGATCTMAATGGCTCCAAAGAAAGCCGGGATATGTGAGTGAAGTGAAGCAAC	15066
Db	1056	GCAACCCCTTTGGATCTMAATGGCTCCAAAGAAAGCCGGGATATGTGAGTGAAGTGAAGCAAC	11115
QY	1507	CCAAGCCCGCTCCACTCCCGCAGTGAACGCCCGGCGCGGGCGCGGGCGTTCGAAC	1566
Db	1116	CCAAGCCCGCTCCACTCCCGCAGTGAACGCCCGGCGCGGGCGCGGGCGTTCGAAC	1175
QY	1567	CGCGGGGCGGAGAGCCGAGCTTCGGGGCGCGGTTCGGCGCGGAGCTCAAGAGTTCTTGCGCT	1626
Db	1176	CGCGGGGCGGAGAGCCGAGCTTCGGGGCGCGGTTCGGCGCGGAGCTCAAGAGTTCTTGCGCT	1235
QY	1627	GGCTCAAGAAACAGACCGTACTGTCTCCAACTCCAGCTTCGGCTCTCAAGACAGTGGCGAG	1686
Db	1236	GGCTCAAGAAACAGACCGTACTGTCTCCAACTCCAGCTTCGGCTCTCAAGACAGTGGCGAG	1235
QY	1687	CCTGATGTCAGAAATGTCGACAAAGACCCGCAACCAAGACGAGGGAGATCTGCTTCGGGCA	1746
Db	1296	CCTGATGTCAGAAATGTCGACAAAGACCCGCAACCAAGACGAGGGAGATCTGCTTCGGGCA	1355
QY	1747	GACGGGGGACGCGCCGAGAGGTCTCTGCAATTAAGCTGTAGGGGCTCAAGGCCAACCTCCCTG	1806
Db	1356	GACGGGGGACGCGCCGAGAGGTCTCTGCAATTAAGCTGTAGGGGCTCAAGGCCAACCTCCCTG	1415
QY	1807	CCACGTGAGACGCGAGAGGCCGAACCCAACTGGGGCCACTCTGTACCTCACTTCAGG	1866
Db	1416	CCACGTGAGACGCGAGAGGCCGAACCCAACTGGGGCCACTCTGTACCTCACTTCAGG	1475
QY	1867	GCACCTGAGCCACCTCTCAGCAGAGAGCTGGGGTGCCCTTGAGCTCCAAAGGCAATACAG	1922
Db	1476	GCACCTGAGCCACCTCTCAGCAGAGAGCTGGGGTGCCCTTGAGCTCCAAAGGCAATACAG	1533
QY	1927	CTCTGACTCCACCGTAGAGGCCACCTTGGGTGCACCCGAGTGGGTGTGTGTGTGTG	1986
Db	1536	CTCTGACTCCACCGTAGAGGCCACCTTGGGTGCACCCGAGTGGGTGTGTGTGTGTGTG	1593
QY	1987	AGGGTTGGTTGAGTTGCTTAGAACCTCTGCCAGGCTGGGGGTGAGAAAGGGAGTCATTA	2046
Db	1596	AGGGTTGGTTGAGTTGCTTAGAACCTCTGCCAGGCTGGGGGTGAGAAAGGGAGTCATTA	165
QY	2047	CTCCCATTTACTTAGGGGCCCTCTCCAAAAGA	2076
Db	1656	CTCCCATTTACTTAGGGGCCCTCTCCAAAAGA	1685
RESULT 3			
AC	ABQ88149	ABQ88149 standard; cDNA; 1716 BP.	
XX	ABQ88149;		
DT	18-SEP-2002	(first entry)	
DE	Human osteoblast differentiation related cDNA SEQ ID NO 56.		
XX	Human; osteoblast; stem cell differentiation; bone tissue deposition;		
KW	osteoporosis; osteopathic; ss.		
OS	Homo sapiens.		
PN	WO200250301-A2.		
PD	27-JUN-2002.		
PF	18-DEC-2001; 2001WO-US048276.		
PR	18-DEC-2000; 2000US-0255882P.		
PR	24-APR-2001; 2001US-0285691P.		
PA	(GENE-) GENE LOGIC INC.		
PA	(PROC) PROCTER & GAMBLE CO.		
XX			

Query Match	Best Local Similarity	Matches 1586; Conservative	75.6%; 99.7%	Score 1572.4; Pred. No. of Mismatches 0;	DB 6; Length 1716; 1; Indels 3; Gaps 1;
QY	490	GC	GC	GC	GC
DB	96	GC	GC	GC	GC
QY	550	CG	CG	CG	CG
DB	156	CG	CG	CG	CG
QY	607	GAG	GAG	GAG	GAG
DB	216	GAG	GAG	GAG	GAG
QY	667	GCT	GCT	GCT	GCT
DB	276	GCT	GCT	GCT	GCT
QY	727	GCT	GCT	GCT	GCT
DB	336	GCT	GCT	GCT	GCT
QY	787	CCT	CCT	CCT	CCT
DB	396	CCT	CCT	CCT	CCT
QY	847	ACT	ACT	ACT	ACT
DB	456	ACT	ACT	ACT	ACT
QY	907	TGC	TGC	TGC	TGC
DB	516	TGC	TGC	TGC	TGC
QY	967	GCG	GCG	GCG	GCG
DB	576	GCG	GCG	GCG	GCG
QY	1027	ACA	ACA	ACA	ACA

Db 636 ACAAGCTTAAAGTGTATGCGCAGAGCAACATGATGAGAGTACCAACAGATGGGGCCCC 695
 QY 1087 ACTGCTGCAATGCTCCCAAGGACCTGGCTCTTTAGCCCTTAAGATCTGGGTGAGG 1146
 Db 696 ACTCTGCAATGCTCCCAAGGACCTGGCTCTTTAGCCCTTAAGATCTGGGTGAGG 755
 QY 1147 CCACCAACCGGCTGGCTGCTCCGCTCCGATGATCAACCGCTGGATCTCTGGATG 1206
 Db 756 CCACCAACCGGCTGGCTGCTCCGCTCCGATGATCAACCGCTGGATCTCTGGATG 815
 QY 1207 TGACACGAGACCCCGCCGACGTCAGTCGAGCCGCTGGGGGCTGAGAGACAC 1266
 Db 816 TGACACGAGACCCCGCCGACGTCAGTCGAGCCGCTGGGGGCTGAGAGACAC 875
 QY 1267 TGAGCGTGGCTGGGTGTGCGCACCCGCTCAAGATTTCTTTCAACCCCAATAC 1326
 Db 876 TGAGCGTGGCTGGGTGTGCGCACCCGCTCAAGATTTCTTTCAACCCCAATAC 935
 QY 1327 AGATCCGCTACCGAGTGAAGAGACAGTGTGACTGGAAGTGTGAGACGATGAGCAAC 1386
 Db 936 AGATCCGCTACCGAGTGAAGAGACAGTGTGACTGGAAGTGTGAGACGATGAGCAAC 995
 QY 1387 AGATCCCTCTGCGCTGCGCTGCGCTGAAACCCGCGACCGTGTACTTGTGCAAGTGGCT 1446
 Db 996 AGATCCCTCTGCGCTGCGCTGCGCTGAAACCCGCGACCGTGTACTTGTGCAAGTGGCT 1055
 QY 1447 GCAACCCCTTTGGATCTATGCTTCCAAAGAACCCGGATTTGGAGTGTGAGACCAAC 1506
 Db 1056 GCAACCCCTTTGGATCTATGCTTCCAAAGAACCCGGATTTGGAGTGTGAGACCAAC 1115
 QY 1507 CCAAGACCGGCTCTCACTCCCGCAGTGAAGCCGCGGCGCGGCGCGCGCGCTGCGGAC 1566
 Db 1116 CCAAGACCGGCTCTCACTCCCGCAGTGAAGCCGCGGCGCGGCGCGCGCTGCGGAC 1175
 QY 1567 CGCGGGCGGAGAGACCGAGCTCGGGGCGGATGCGGCGGAGCTCAAGCATTTCTGGGCT 1626
 Db 1176 CGCGGGCGGAGAGACCGAGCTCGGGGCGGATGCGGCGGAGCTCAAGCATTTCTGGGCT 1235
 QY 1627 GGCTCAAGAGACGAGCTATGCTTCCAAACCTCACTTCCGCTCTTACGACCAAGTGGGAG 1686
 Db 1236 GGCTCAAGAGACGAGCTATGCTTCCAAACCTCACTTCCGCTCTTACGACCAAGTGGGAG 1295
 QY 1687 CTTGATGCAAGATGTCACAAAGACCGGCAACGAGAGGAGCTGCGCTCGGGACA 1746
 Db 1296 CTTGATGCAAGATGTCACAAAGACCGGCAACGAGAGGAGCTGCGCTCGGGACA 1355
 QY 1747 GACGGGGCAGCGGCGAGAGTCTGCAAGATTAAGCTGTAGGGGCTCAAGGCCACCTTCTCTG 1806
 Db 1356 GACGGGGCAGCGGCGAGAGTCTGCAAGATTAAGCTGTAGGGGCTCAAGGCCACCTTCTCTG 1415
 QY 1807 CCAAGTGAAGACGAGAGGCGGAAACCAACTGGGGGCACTCTGTACCTTCACTTCAAG 1866
 Db 1416 CCAAGTGAAGACGAGAGGCGGAAACCAACTGGGGGCACTCTGTACCTTCACTTCAAG 1475
 QY 1867 GCACCTGAGCACCCTGACGAGAGTGGGGTGGCCCTGAGCTCCAACGGCCATAACAG 1926
 Db 1476 GCACCTGAGCACCCTGACGAGAGTGGGGTGGCCCTGAGCTCCAACGGCCATAACAG 1535
 QY 1927 CTCTGACTCCCACTGAGGCGCACTTTGGGTGACCCCAAGTGTGTGTGTGTGTGTG 1986
 Db 1536 CTCTGACTCCCACTGAGGCGCACTTTGGGTGACCCCAAGTGTGTGTGTGTGTGTG 1595
 QY 1987 AGGGTTGGTGAAGTGGCTTGAAGACCTTCCAGAGGCTGGGGGTGAGAAAGGAGATCTTA 2046
 Db 1596 AGGGTTGGTGAAGTGGCTTGAAGACCTTCCAGAGGCTGGGGGTGAGAAAGGAGATCTTA 1655
 QY 2047 CTCCCAATTAAGTGGGCGCCCTCCAAAGA 2076
 Db 1656 CTCCCAATTAAGTGGGCGCCCTCCAAAGA 1685

ID ABX14013 standard; cDNA; 1716 BP.
 XX
 AC ABX14013;
 XX
 DT 20-FEB-2003 (first entry)
 XX
 DE Human cytokine receptor-like factor 1 (CLF-1 or CLRf-1) cDNA.
 XX
 KW Human; gene; ss; gene expression; bone formation; cartilage formation;
 KW embryonic development; cytokine receptor-like factor 1; CLF-1; CLRf-1;
 KW mesenchymal cell differentiation; matrix metalloproteinase 23; MMP23;
 KW bone development; antagonist; agonist; cadherin; CD68; cytokine;
 KW diagnosis; osteodystrophy; osteopetrosis; osteoblastoma;
 KW osteopetrosis; osteogenesis imperfecta; osteoporosis; osteopenia;
 KW osteoma; osteoblastoma; periodontal disease; hyperparathyroidism;
 KW hypercalcaemia of malignancy; Paget's disease; osteolytic lesion;
 KW bone metastasis; bone loss; immobilisation; sex hormone deficiency;
 KW inflammatory disease; rheumatoid arthritis; osteoarthritis;
 KW bone fracture.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 119..1387
 FT /*tag= a
 FT /product= "CLF-1"
 FT
 XX W0200285285-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002MO-US012149.
 XX
 PR 18-APR-2001; 2001US-0284786P.
 XX
 PA (MHP) WYETH.
 XX
 PI Clancy B, Pittman DM;
 XX WPI; 2003-103384/09.
 DR P-PSDB; ABG72776.
 DR
 XX
 PT Determining the difference between levels of expression of a number of
 PT genes; useful for diagnosing and treating disorders associated with bone
 PT or cartilage formation or resorption such as osteoporosis and bone
 PT fractures.
 XX
 PS Disclosure; Page 190-192; 197tp; English.
 XX
 CC The invention discloses a method for determining the difference between
 CC the levels of expression of a number of, at least 500 genes, during bone
 CC or cartilage formation. The method comprises determining levels of RNA
 CC from the genes to obtain levels of expression and comparing these to a
 CC set of reference levels for each of the genes. Bone formation is an
 CC essential process in embryonic development and plays a critical role in
 CC many diseases and conditions in humans. Two genes found to be regulated
 CC during bone and cartilage formation are the cytokine receptor-like factor
 CC 1 (CLF-1 or CLRf-1), which is specifically regulated during mesenchymal
 CC cell differentiation, and matrix metalloproteinase 23 (MMP23), which is
 CC specifically regulated during bone development. Also disclosed is a
 CC computer program for analysing levels of expression of a number of genes,
 CC comprising a number of antagonists or agonists of the genes
 CC and methods for determining whether a subject has, or is likely to
 CC develop, a disease related to bone or cartilage resorption or formation,
 CC for determining the effectiveness of a treatment intended to stimulate
 CC bone or cartilage formation or resorption, for identifying a compound for
 CC treating, modulating or stimulating a disease related to bone or
 CC cartilage formation possibly acting as a cadherin or CD68 agonist or a
 CC cytokine antagonist. The methods and compositions are useful for
 CC diagnosing and treating disorders associated with bone or cartilage
 CC formation or resorption such as osteodystrophy, osteopetrosis,
 CC osteoblastoma, osteopetrosis, osteogenesis imperfecta, osteoporosis,
 CC osteopenia, osteoma and osteoblastoma, periodontal disease,

Db 953 AGATCCGCTACCGAGTGGAGGACAGTGTGACTGGAGGTGGTGGACATGTGGACCAACC 1012
1387 AGACCTCCCTGCGCGCTGCGCGCTGAAACCCGCGACCCGTGTATCTTGTGCAAGTGGCT 1446
1013 ABACTCTCCGCGCGCTGCGCGCTGAAACCCGCGACCCGTGTATCTTGTGCAAGTGGCT 1072
1447 GCAACCCCTTTGGCATCTATGTGCTCCAGAAAGCCGGGATCTGAGTGAAGTGAAGCCACC 1506
1073 GCAACCCCTTTGGCATCTATGTGCTCCAGAAAGCCGGGATCTGAGTGAAGTGAAGCCACC 1132
1507 CCAACGCGCGCTCCCACTCCCGCAGTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1566
1133 CCAACGCGCGCTCCCACTCCCGCAGTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1192
1567 CCGCGCGCGCGAGAGCGCGAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1626
1193 CCGCGCGCGCGAGAGCGCGAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1252
1627 GGTCTCAAGAGCAAGCGGTACTGTCTCAACCTTCCGCTCTTCAAGTGAAGTGAAGCCACC 1686
1253 GGTCTCAAGAGCAAGCGGTACTGTCTCAACCTTCCGCTCTTCAAGTGAAGTGAAGCCACC 1312
1687 CCTGATGAGAGAGTGCACAAAGCCCGCAACGAGGAGGAGTCTGCGCGCGCGCGCGCGCG 1746
1313 CCTGATGAGAGAGTGCACAAAGCCCGCAACGAGGAGGAGTCTGCGCGCGCGCGCGCGCG 1372
1747 GACGGGGGACCGGGAGAGGTCTCTGCGAGATTAAGCTGTAGGGGCTCAGGCCACCTCCCTG 1806
1373 GACGGGGGACCGGGAGAGGTCTCTGCGAGATTAAGCTGTAGGGGCTCAGGCCACCTCCCTG 1432
1807 CCACTGTGAGAGCGCAAGAGGCTCCCAACCTGGGGGCGACCTGTATACCTCACTTCAAG 1866
1433 CCACTGTGAGAGCGCAAGAGGCTCCCAACCTGGGGGCGACCTGTATACCTCACTTCAAG 1492
1867 GCACTGTGAGAGCGCTCAGAGAGGCTGGGGTGGCGCTGAGCTCCCAAGCGCCATTAACAG 1926
1493 GCACTGTGAGAGCGCTCAGAGAGGCTGGGGTGGCGCTGAGCTCCCAAGCGCCATTAACAG 1552
1927 CTCTGACTCCCAAGTGAAGCGCACTTGGGTGCAAGCGCGGTGTGTGTGTGTGTGTGTGT 1986
1553 CTCTGACTCCCAAGTGAAGCGCACTTGGGTGCAAGCGCGGTGTGTGTGTGTGTGTGTGT 1612
1987 AGGCTGTGTGAGTGTGCTTGAAGACCTCTGCAAGGCGTGGGGGTGAGAGGGGAGTCACTTA 2046
1613 AGGCTGTGTGAGTGTGCTTGAAGACCTCTGCAAGGCGTGGGGGTGAGAGGGGAGTCACTTA 1672
2047 CTCTCCATTACCTTGAAGGCGCGCTCCAAAGA 2076
1673 CTCTCCATTACCTTGAAGGCGCGCTCCAAAGA 1702

RESULT 8
AA80050
ID AA80050 standard; cDNA; 1789 BP.
XX
AC AA80050;
XX
DT 12-AUG-1999 (first entry)
XX
DE Human PRO327 nucleotide sequence.
XX
KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
KW secreted protein; transmembrane protein; inflammation disorder; ss.
XX
XX Homo sapiens.
XX OS
XX PN WO9228462-A2.
XX
PD 10-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US025108.
XX

PR 03-DEC-1997; 97US-0067411P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069333P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 16-DEC-1997; 97US-0069694P.
PR 16-DEC-1997; 97US-0069702P.
PR 16-DEC-1997; 97US-0069870P.
PR 17-DEC-1997; 97US-0069873P.
PR 18-DEC-1997; 97US-0068017P.
PR 05-JAN-1998; 98US-0070440P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-FEB-1998; 98US-0075945P.
XX
XX (GENTH) GENENTECH INC.
XX
XX PA
XX PI Wood WI, Goddard A, Gurney AL, Yuan J, Baker KP, Chen J;
XX DR WPI, 1999-371118/31.
XX DR P-PSDB; AAT17825.
XX
XX PS Nucleic acids encoding PRO secreted and transmembrane proteins.
XX
XX Claim 2; Fig 16; 123pp; English.
XX
XX The present invention describes nucleic acids encoding PRO secreted and
XX transmembrane proteins used therapeutically. The PRO proteins have
XX cytosolic, anti-inflammatory, anti-proliferative and immunosuppressive
XX activity. The proteins and polynucleotides can be used in therapy,
XX identification of homologues, raising antibodies and design of probes and
XX primers. They can be used in a range of diseases related to proteins that
XX they have homology with, e.g. a PRO protein having homology to complement
XX proteins may be used in inflammatory responses
SQ Sequence 1789 BP; 358 A; 624 C; 529 G; 278 T; 0 U; 0 Other;
Query Match 75.6%; Score 1572.4; DB 2; Length 1789;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1586; Conservative 0; Mismatches 1; Indels 3; Gaps 1;
QY 490 GCGCCCGCGGACG 549
DB 96 GCGCCCGCGGACG 155
QY 550 CCG 606
DB 156 CCG 215
QY 607 GAGCGCGGATCAGAGAGCGCAAGAGTGTATGATCCCAAGATCCCAAGTCTTCATCG 666
DB 216 GAGCGCGGATCAGAGAGCGCAAGAGTGTATGATCCCAAGATCCCAAGTCTTCATCG 275
QY 667 GCTCTCTCTGTGCGCACTGTGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726
DB 276 GCTCTCTCTGTGCGCACTGTGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 335
QY 727 GCTCTCTCTGTGCGCACTGTGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
DB 336 GCTCTCTCTGTGCGCACTGTGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 395
QY 787 CTTCCACTTGTGCTGTGCG 846
DB 396 CTTCCACTTGTGCTGTGCG 455
QY 847 ACTGTGTGTGCAAGCG 906
DB 456 ACTGTGTGTGCAAGCG 515
QY 907 TGGCCCGAGAGAAACCGCTCAATCACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 966
DB 516 TGGCCCGAGAGAAACCGCTCAATCACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 575

Db 1176 CGCGGGGCGAGAGAGCCAGGCTCGGGGCGGGGCGGAGCTCAAGAGTCTCTGGGCT 1235
 Qy 1627 GGCTCAAGAGAGAGAGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 1686
 Db 1236 GGGCTCAAGAGAGAGAGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 1295
 Qy 1687 CCTGATGCAAGAGAGAGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 1746
 Db 1296 CCTGATGCAAGAGAGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 1355
 Qy 1747 GACGGGCGAGAGAGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 1806
 Db 1356 GACGGGCGAGAGAGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 1415
 Qy 1807 CCAAGTGAAGAGAGAGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 1866
 Db 1416 CCAAGTGAAGAGAGAGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 1475
 Qy 1867 GCAAGTGAAGAGAGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 1926
 Db 1476 GCAAGTGAAGAGAGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 1535
 Qy 1927 CTCTGACTCCAGAGAGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 1986
 Db 1536 CTCTGACTCCAGAGAGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 1595
 Qy 1987 AGGGTTGGTGAAGTGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 2046
 Db 1596 AGGGTTGGTGAAGTGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 1655
 Qy 2047 CTCCCATTAAGAGAGGCTGCTGCTCAAGCA 2076
 Db 1656 CTCCCATTAAGAGAGGCTGCTGCTCAAGCA 1685

RESULT 12

ABX96790
 ID ABX96790 standard; cDNA; 1790 BP.
 AC ABX96790;
 XX
 DT 15-MAY-2003 (first entry)
 XX

Human cDNA encoding secreted/transmembrane protein PRO327.

XX Human; ss; gene; PRO; secreted protein; transmembrane protein;
 KM Cornelia de Lange syndrome; gene therapy; immune disorder;
 KM inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KM infertility; birth defect; premature aging; cardiac injury; AIDS; cancer;
 KM diabetic complication.

XX Homo sapiens.

XX OS US2002173463-A1.

XX PD 21-NOV-2002.

XX PF 31-AUG-2001; 2001US-00944944.

XX PR 03-DEC-1997; 97US-0067411P.

XX PR 11-DEC-1997; 97US-0069278P.

XX PR 11-DEC-1997; 97US-0069334P.

XX PR 12-DEC-1997; 97US-0069425P.

XX PR 16-DEC-1997; 97US-0069694P.

XX PR 16-DEC-1997; 97US-0069696P.

XX PR 17-DEC-1997; 97US-0069702P.

XX PR 17-DEC-1997; 97US-0069870P.

XX PR 18-DEC-1997; 97US-0069873P.

XX PR 05-JAN-1998; 98US-0070440P.

XX PR 09-FEB-1998; 98US-0074086P.

PR 09-FEB-1998; 98US-0074092P.
 PR 25-FEB-1998; 98US-0075945P.
 PR 16-SEP-1998; 98MO-US019330.
 PR 01-DEC-1998; 98MO-US025108.
 PR 16-DEC-1998; 98US-0112850P.
 PR 22-DEC-1998; 98US-0113296P.
 PR 02-JUN-1999; 99MO-US012252.
 PR 28-JUL-1999; 99US-0146222P.
 PR 15-SEP-1999; 99MO-US021090.
 PR 30-NOV-1999; 99MO-US028513.
 PR 30-NOV-1999; 99MO-US028513.
 PR 01-DEC-1999; 99MO-US028513.
 PR 16-DEC-1999; 99MO-US030095.
 PR 11-FEB-2000; 2000MO-US003565.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 02-MAR-2000; 2000MO-US005841.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 28-JUL-2000; 2000MO-US020710.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 28-FEB-2001; 2001MO-US006520.
 PR 25-MAY-2001; 2001US-00866028.

XX (GENTH) GENENTECH INC.

XX PI Baker KP, Botstein D, Eaton DL, Ferrara N, Flivaroff E;

XX PI Gierlisen ME, Goddard A, Godowski PU, Grimaldi UC, Gurney AL;

XX PI Hillan KJ, Kljavin ID, Napier MA, Roy MA, Tumas D, Wood WT;

XX DR WPI; 2003-311003/30.

XX PT P-PSDB; ABU64921.

XX PS Claim 2; Fig 13; 172pp; English.

XX CC The invention relates to an isolated nucleic acid encoding a secreted/
 CC transmembrane polypeptide (designated as PRO proteins). 15 PRO
 CC polypeptides and their encoding polynucleotides are disclosed. Also
 CC included are a vector comprising the PRO nucleic acid, a host cell
 CC comprising the vector, a process for producing a PRO polypeptide (by
 CC culturing the host cell under conditions for the expression of the PRO
 CC polypeptide, and recovering the PRO polypeptide from the cell culture,
 CC the PRO polypeptide having at least 80% amino acid sequence identity to
 CC the PRO polypeptides, a chimeric molecule comprising PRO fused to a
 CC heterologous amino acid sequence and an antibody which specifically binds
 CC to PRO. The PRO nucleotide sequences are useful as hybridisation probes,
 CC in chromosome and gene mapping, in generating sense and antisense RNA or
 CC DNA, in generating transgenic or knock-out animals which can be used in
 CC the development and screening of therapeutically useful reagents, and in
 CC gene therapy. The polypeptides may be used as molecular weight markers
 CC for protein electrophoresis purposes. The PRO polypeptides and nucleic
 CC acids may also be used for chromosome identification, and tissue typing.
 CC PRO241 (identified as Chordin) is a candidate gene for Cornelia de Lange
 CC syndrome. Other PRO proteins are variously implicated in immune
 CC disorders, inflammatory disease, organ failure, atherosclerosis, cardiac
 CC injury, infertility, birth defects, premature aging, cardiac injury,
 CC AIDS, cancer and diabetic complications. The present sequence encodes a
 CC PRO protein

XX SQ Sequence 1790 BP; 359 A; 624 C; 529 G; 278 T; 0 U; 0 Other;

XX Query Match 75.6%; Score 1572.4; DB 8; Length 1790;

XX Best Local Similarity 99.7%; Pred. No. 0;

XX Matches 1586; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy 490 GCGCCCCGCGAGAGAGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 549

Db 96 GCGCCCCGCGAGAGAGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 155

Qy 550 CGCGGGGCGAGAGAGGCTGCTGCTCAAGCTTCCGCTCTTACAGCAAGTGGGAG 606

QY 1927 CTCGACCTCCACGTCAGGACCACTTTGGGTGCACCCGATGAGTGTGTGTGTGTG 1986
DB 1536 CTCGACTCCACGTCAGGACCACTTTGGGTGCACCCGATGAGTGTGTGTGTGTG 1595
QY 1987 AAGGTTGGTGTGAGTGTGCTTGAACCCCTGCGGCTGGGGGTGAAGAGGAGTCATT 2046
DB 1596 AAGGTTGGTGTGAGTGTGCTTGAACCCCTGCGGCTGGGGGTGAAGAGGAGTCATT 1655
QY 2047 CTCGCCATTACCTAGGGGCCCCCTCCAAAGA 2076
DB 1656 CTCGCCATTACCTAGGGGCCCCCTCCAAAGA 1685

RESULT 14
ABX7078
ID ABX7078 standard; cDNA; 1790 BP.

ABX7078;
04-APR-2003 (first entry)
cDNA sequence encoding human PRO327 protein.

Gene: ss; human; anti-inflammatory; antiarteriosclerotic; cardiant;
anti-inflammatory; anti-HIV; cytostatic; antidiabetic; transmembrane;
anti-inflammatory; cytostatic; antidiabetic; gene therapy; birth defect;
inflammatory disease; organ failure; atherosclerosis; cardiac injury;
premature aging; AIDS; cancer; diabetic complication.

OS Homo sapiens.

XX US2002142958-A1.

XX 03-OCT-2002.

XX 30-AUG-2001; 2001US-00943762.

XX 16-SEP-1998; 98WO-US019330.
PR 01-DEC-1998; 98WO-US025108.
PR 22-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 25-MAY-2001; 2001US-00866028.

XX (GENTH) GENENTECH INC.

XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
PI Gerltsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
XX WPI; 2003-174140/17.
XX P-PSDB; ABUS7242.

XX New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.

XX Claim 2; Fig 13; 173pp; English.

CC This invention relates to a nucleotide sequence encoding an isolated
CC secreted and/or transmembrane protein. The nucleotide sequences of the
CC invention may have anti-inflammatory, antiarteriosclerotic, cardiant, anti
CC -infertility, anti-HIV, cytostatic and antidiabetic activities and may be
CC used in gene therapy. The nucleic acids and polypeptides are useful for
CC treating inflammatory diseases, organ failure, atherosclerosis, cardiac
CC injury, infertility, birth defects, premature aging, AIDS, cancer, or
CC diabetic complications. The nucleic acids are useful as hybridisation
CC probes, in chromosome and gene mapping, and in generating antisense RNA
CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
CC biosensors or bioreactors. Both are useful in tissue typing. The present
CC sequence represents a nucleic acid sequence of the invention

XX SQ Sequence 1790 BP; 359 A; 624 C; 529 G; 278 T; 0 U; 0 Other;

Query Match 75.6%; Score 1572.4; DB 8; Length 1790;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1586; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 490 GCGCCCGGAGCGCGCGCCCAATGCGCGCGCGCGCGCGCGCGCGCCCAATCG 549
DB 96 GCGCCCGGAGCGCGCGCCCAATGCGCGCGCGCGCGCGCGCGCGCCCAATCG 155
QY 550 CG 606
DB 156 CG 215
QY 607 GAGCGGATCAGAGACCCCAACAGTGTGATCAGTCCCAAGATCCCAAGTTCATCG 666
DB 216 GAGCGGATCAGAGACCCCAACAGTGTGATCAGTCCCAAGATCCCAAGTTCATCG 275
QY 667 GCTCTCTCTGTCGACCTGCTCAGTGCAGAGACCCCAAGATCCCAAGTTCATCG 726
DB 276 GCTCTCTCTGTCGACCTGCTCAGTGCAGAGACCCCAAGATCCCAAGTTCATCG 335
QY 727 GCTCTCTCTGTCGACCTGCTCAGTGCAGAGACCCCAAGATCCCAAGTTCATCG 786
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QY 787 CCTCCACCTTGGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 846
DB 396 CCTCCACCTTGGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 455
QY 847 ACCTGCTGTCAGCG 906
DB 456 ACCTGCTGTCAGCG 515
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DB 516 TGCCTCCAGAGAACCCGTCATCATGCTGCTGCTCAAGAACATGAAGACTTGACT 575
QY 967 GCGCGTCGACGCGCAGAGGCGCGCAGAGGAGACCTTCTCCACAGCACTCAAGT 1026
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QY 1027 ACAAGCTTAGTGTGATGTCGACGACCAACATGTAAGAGTACCAACAGTGGGCGCC 1086
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DB 696 ACTCTGTCACATCCCAAGAGACTGCGCTCTTTACGCGCCCTATGAGATCTGGTGAAG 755
QY 1147 CCACCAACG 1206
DB 756 CCACCAACG 815
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QY 1267 TGAACG 1326

Db 876 TGAAGTCGCGTGGGTTCGCAACCCGCTCAAGATTCTCTTTCMAAGCAATAACC 935
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 Db 1236 GCGCTCAAGAAAGCAGCTGCTCAAGCTTCCGCTCTTACGACCAAGTGGCGAG 1295
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 Qy 1747 GACGCGGCGACGCGGAGAGTCTTCCGCAAGATTAAGCTGTAGGGGCTCAAGCCACCTCCCTG 1806
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 Db 1536 CTCTGACTCCAGGTGAGGCGACCTTTGGGTGACCCCACTGGGTGTGTGTGTGTGTG 1595
 Qy 1987 AGCGTTGGTGTGAGTGTGCTTAAGAACCCCTGTCAGGGCTGGGGGTGAGAAAGGAGTCAATTA 2046
 Db 1596 AGCGTTGGTGTGAGTGTGCTTAAGAACCCCTGTCAGGGCTGGGGGTGAGAAAGGAGTCAATTA 1655
 Qy 2047 CTCCCAATTACCTAAGGCGCCCTCCAAAGA 2076
 Db 1656 CTCCCAATTACCTAAGGCGCCCTCCAAAGA 1685
 RESULT 15
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 ID ABX75909 standard; cDNA; 1790 BP.
 XX
 AC ABX75909;
 XX
 DT 31-MAR-2003 (first entry)
 XX
 DE Human cDNA encoding secreted/transmembrane protein, PRO327.
 XX
 KW Human; ss; gene; PRO; antiinflammatory; antiarteriosclerotic; cardiac;
 KW gynecological; anti-HIV; cytostatic; antidiabetic; inflammatory disease;
 KW organ failure; atherosclerosis; cardiac injury; infertility;
 KW birth defect; premature aging; AIDS; acquired immunodeficiency syndrome;
 KW cancer; diabetic complication.
 XX
 OS Homo sapiens.
 XX

PN US2002132981-A1.
 XX
 PD 19-SEP-2002.
 XX
 PF 30-AUG-2001; 2001US-00944396.
 XX
 PR 03-DEC-1997; 97US-0067411P.
 PR 11-DEC-1997; 97US-0069278P.
 PR 11-DEC-1997; 97US-0069334P.
 PR 11-DEC-1997; 97US-0069335P.
 PR 12-DEC-1997; 97US-0069425P.
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 PR 18-DEC-1997; 97US-0068017P.
 PR 05-JAN-1998; 98US-0070440P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-FEB-1998; 98US-0075945P.
 PR 16-SEP-1998; 98WO-US019330.
 PR 01-DEC-1998; 98WO-US025108.
 PR 16-DEC-1998; 98US-0112850P.
 PR 22-DEC-1998; 98US-0113296P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 28-JUL-1999; 99US-0146222P.
 PR 15-SEP-1999; 99WO-US021090.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028401.
 PR 16-DEC-1999; 99WO-US030095.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 25-MAY-2001; 2001US-00866028.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Eaton DL, Ferrara N, Flvaroff E,
 PI Gerltsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
 PI Hillan KJ, Kijavini IV, Napier MA, Roy MA, Tumas D, Wood WI;
 XX
 DR WPI; 2003-147446/14.
 DR P-Psdb; ABUS6306.
 XX
 PT New isolated PRO polypeptide and encoding nucleic acids, useful for the
 PT diagnosis and treatment of disorders such as inflammatory disease,
 PT atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic
 PT complications.
 XX
 PS Claim 2; Fig 13; 171pp; English.
 XX
 CC The invention relates to an isolated PRO polypeptide having at least 80%
 CC amino acid sequence identity to and scoring at least 80% positives when
 CC compared to any of 15 fully defined sequences of 235-954 amino acids,
 CC given in the specification. Also included are: (1) an isolated PRO
 CC nucleic acid having at least 80% nucleic acid sequence identity to a
 CC nucleotide sequence that encodes PRO or its extracellular domain, and
 CC comprising any of 15 fully defined nucleotide sequences of 957-3441 bp,
 CC given in the specification and deposited under ATCC accession number
 CC 209526, 209508, 209524, 209528, 209530, 209523, 209492, 209532, 209531,
 CC 209529, 209527, 209570, 209618, 209621 and 209619; (2) a vector
 CC comprising the PRO nucleic acid; (3) a host cell comprising the vector;
 CC (4) producing PRO polypeptides, comprising culturing the cell for
 CC expression of the PRO polypeptide and recovering the PRO polypeptide from
 CC the cell culture; (5) a chimeric molecule comprising PRO fused to a
 CC heterologous amino acid sequence; and (6) an anti-PRO antibody. The

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2005, 14:43:56 ; Search time 1103 Seconds
(without alignments)
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Searched: 5394803 seqs, 2962729879 residues

Total number of hits satisfying chosen parameters: 10789606

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1572.4	75.6	1716	17	US-10-329-056-1
6	1572.4	75.6	1716	18	US-10-450-826-56
7	1572.4	75.6	1790	9	US-09-866-028-51
8	1572.4	75.6	1790	9	US-09-944-449-31
9	1572.4	75.6	1790	9	US-09-944-457-31
10	1572.4	75.6	1790	9	US-09-945-587-31
11	1572.4	75.6	1790	9	US-09-945-015-31

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38	1572.4	75.6	2154	18	US-10-723-860-6062	Sequence 6062, Ap
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ALIGNMENTS

RESULT 1

US-09-037-657-43

Sequence 43, Application US/09037657A

Patent No. US20020045741A1

GENERAL INFORMATION:

APPLICANT: Hilton, Douglas J.

APPLICANT: Nicola, Nicob A.

APPLICANT: Farley, Alison

APPLICANT: Wilson, Tracy

APPLICANT: Zhang, Jian-Guo

APPLICANT: Alexander, Warren

APPLICANT: Rakar, Steven

APPLICANT: Fabril, Louis

APPLICANT: Kojima, Tetsuo

APPLICANT: Maeda, Masatsugu

APPLICANT: Kikuchi, Yasufumi

APPLICANT: Naeb, Andrew

TITLE OF INVENTION: A NOVEL HAEMOPIETIN RECEPTOR AND GENETIC SEQUENCES

FILE REFERENCE: DAVIES COLLISON CAVE (CIP)

CURRENT APPLICATION NUMBER: US/09/037,657A

CURRENT FILING DATE: 1998-03-10

EARLIER APPLICATION NUMBER: 08/928,720

EARLIER FILING DATE: 1997-09-11

NUMBER OF SEQ ID NOS: 54

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 43

LENGTH: 2079

TYPE: DNA

ORGANISM: Unknown

NAME/KEY: CDS

LOCATION: (513) ..(1775)

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Nucleotide Sequence of NR6
US-09-037-657-43

Query Match 100.0%; Score 2079; DB 9; Length 2079;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2079; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 721 CCGAGGGCCCTTATGAGAGCCCTCAATGGGGGCGCGCGCGCGCGCGCGCGCGCGCG 780
DB 721 CCGAGGGCCCTTATGAGAGCCCTCAATGGGGGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 781 TCAACGCTCTCACTTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
DB 781 TCAACGCTCTCACTTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 841 GGGAGCAACTCTGTGTGCGCAAGCCCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GGGAGCAACTCTGTGTGCGCAAGCCCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 TTGGCTTGGCCCCAGAGAAACCGGTCAATGAGCTGTGCTGCTCAAGAACTAAGAGACT 960
DB 901 TTGGCTTGGCCCCAGAGAAACCGGTCAATGAGCTGTGCTGCTCAAGAACTAAGAGACT 960
QY 961 TGAAGCTGCGCTGAGAGCGAGGGGCCAGGGGAGAGCTTCTCAACCACTACTGCC 1020
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DB 961 TGAAGCTGCGCTGAGAGCGAGGGGCCAGGGGAGAGCTTCTCTCAACCACTACTGCC 1020
QY 1021 TCAAGTACAGACTTGTAGTGTGTATGTGCGCAGAGACAACTATGTAGAGATCCACAGTGG 1080
DB 1021 TCAAGTACAGACTTGTAGTGTGTATGTGCGCAGAGACAACTATGTAGAGATCCACAGTGG 1080
QY 1081 GGGCCCACTCTGCGCAATCCCAAGAGACTGTGCTCTTTTACGCCCTTATGAGATTCGG 1140
DB 1081 GGGCCCACTCTGCGCAATCCCAAGAGACTGTGCTCTTTTACGCCCTTATGAGATTCGG 1140
QY 1141 TGAAGGCAACAAACGCTGTGAGCTGTGCGCGCTGCGATGTACTCAAGCTGATATCTGG 1200
DB 1141 TGAAGGCAACAAACGCTGTGAGCTGTGCGCGCTGCGATGTACTCAAGCTGATATCTGG 1200
QY 1201 ATGTGTGACCAAGAGACCCCGCGCGAGAGTGCAGTGAAGCGCGCTGAGAGAG 1260
DB 1201 ATGTGTGACCAAGAGACCCCGCGCGAGAGTGCAGTGAAGCGCGCTGAGAGAG 1260
QY 1261 ACCAGCTGAGCGTGGGCTGGGTGTGCGCAACCGCGCTCAAGGATTTCTTTCAAGGCA 1320
DB 1261 ACCAGCTGAGCGTGGGCTGGGTGTGCGCAACCGCGCTCAAGGATTTCTTTCAAGGCA 1320
QY 1321 AATACCAATTCGCTTACCGAGTGAAGAGACAGTGTGACTGGAAGGTGTGAGAGATGTA 1380
DB 1321 AATACCAATTCGCTTACCGAGTGAAGAGACAGTGTGACTGGAAGGTGTGAGAGATGTA 1380
QY 1381 GCAACCAAGCTTCTGCGCGCTGTGCGCGCTGTGAACCGCGCACCGTGTACTTGTGCAAG 1440
DB 1381 GCAACCAAGCTTCTGCGCGCTGTGCGCGCTGTGAACCGCGCACCGTGTACTTGTGCAAG 1440
QY 1441 TGGCTGCAACCCCTTTGGCATCTATGTGCTCAAGAAAGCGGGATCTGAGTGTGTA 1500
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QY 1501 GCCAAGCCCAACAGCGCTTCACTCCCGCAGTGAAGCGCGCGCGCGCGCGCGCGCG 1560
DB 1501 GCCAAGCCCAACAGCGCTTCACTCCCGCAGTGAAGCGCGCGCGCGCGCGCGCGCG 1560
QY 1561 GCGAACCGGGGGCGGAGAGCGAGCTGCGGGCGCGGTGTGCGAGCTCAAGCACTTC 1620
DB 1561 GCGAACCGGGGGCGGAGAGCGAGCTGCGGGCGCGGTGTGCGAGCTCAAGCACTTC 1620
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DB 1621 TGGGCTGTGCTAAGAGAGAGCGGCTACTGCTCAACCTCAAGCTTCCGCTCTGAGCAAGT 1680
QY 1681 GCGAGCGCTGTATGAGAGAGTGCACAAGACCCGCAACAGAGAGAGAGAGAGAGAGTCTG 1740
DB 1681 GCGAGCGCTGTATGAGAGAGTGCACAAGACCCGCAACAGAGAGAGAGAGAGAGAGTCTG 1740
QY 1741 CGGGAGAGCGGGGCAAGCGAGAGGTCTGTGCGAGATGAGCTGTAGGGGCTCAGGCCA 1800
DB 1741 CGGGAGAGCGGGGCAAGCGAGAGGTCTGTGCGAGATGAGCTGTAGGGGCTCAGGCCA 1800
QY 1801 TCCCTGCGCAGTGTGAGAGAGAGAGCGCAAGCCCAATGTGGGGCGCACTGTGATCCCTCAG 1860
DB 1801 TCCCTGCGCAGTGTGAGAGAGAGAGCGCAAGCCCAATGTGGGGCGCACTGTGATCCCTCAG 1860
QY 1861 TTAAGGGGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
DB 1861 TTAAGGGGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 1921 TTAAGAGCTGTGACTCCCAAGTGAAGGCACTTTTGGGTGCAACCCGAGGTGTGTGTG 1980
DB 1921 TTAAGAGCTGTGACTCCCAAGTGAAGGCACTTTTGGGTGCAACCCGAGGTGTGTGTG 1980
QY 1981 TGTGTGAGGGTGTGTGAGTGTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
DB 1981 TGTGTGAGGGTGTGTGAGTGTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
QY 2041 TCATTACTTCCCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
DB 2041 TCATTACTTCCCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
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? PRIOR APPLICATION NUMBER: US 60/284,766
? PRIOR FILING DATE: 2001-04-18
? NUMBER OF SEQ ID NOS: 4
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 1
? LENGTH: 1716
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (119)..(1387)
? OTHER INFORMATION:
US-10-329-056-1

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Query Match	Score	DB	Length
75.6%	1572.4	17	1716

Matches 1586; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY		490	GCGCCCCGAGAGCGCCGGACCCAAATGCCGCAGCCGGCCGGCCCGCCGCAATTCCG	549
Dd		96	GCGTCCCAGAGCGCCGGCCCCAATGCCGCAGCCGGCCCGCCGCAATTCCG	155
QY		550	C G C G A G C G C C G C C G T T G C T G C C C - - - C T G A C T C T C T G C G T C C T C G A G C C G C	606
Dd		156	C G C G A G C G C C C C G C C G T T G C T G C C C C T G A C T C T C T C T G C G T C C T C G A G C C G C	215
QY		607	G A G C C G A T C A G A G C C C A C A G C T G A T C A G T C C C A G A T T C C A C G T T C T A T C G	666
Dd		216	G A G C C G A T C A G A G C C C A C A G C T G A T C A G T C C C A G A T T C C A C G T T C T A T C G	275
QY		667	G C T C T C C C T G C C A C T G C T C A G T C A G A C C C A C A G A G C C A C C G C C A G	726
Dd		276	G C T C T C C C T G C C A C T G C T C A G T C A G A C C C A C A G A G C C A C C G C C A G	335
QY		727	G C C T C T A T G A C C C T C A T G A G G C G C G C C T G C C C C T G A G C T C C C G T G A T C A A G	786
Dd		336	G C C T C T A T G A C C C T C A C A G G G C G C C C T G C C C C T G A C T C C C G T G A C T C A A G	395
QY		787	C C T C A C C T T G A G C C T G G C C C T G G C A A C C T C A N T G G G T C C A G G A G G G T C G G G G A C A	846
Dd		396	C C T C A C C T T G A G C C T G G C C C T G G C A A C C T C A N T G G G T C C A G G A G G G T C G G G G A C A	455
QY		847	A C C T C G T G T G C A C G C C C G T A G C A G C A C A T C T G C T G A G C T C T G C C T C T A T G T T G A C C	906
Dd		456	A C C T C G T G T G C A C G C C C G T A G C A G C A C A T C T G A G C T G A G C T C T G C C T C T A T G T T G A C C	515
QY		907	T G C C C C C A G A A A C C C G T C A A C A T C A G C T G T G T C C A A A A C T A G A A G A C T T T A A C T	966
Dd		516	T G C C C C C A G A A A A C C C G T C A A C A T C A G C T G T G T C C A A A A C A T G A A G A C T T T A A C T	575
QY		967	G C G C T G A C G C C A G G G G C C A C G G G G A G A C T T C C T C A C A C C A A C T A C C C C A A G T	1026
Dd		576	G C G C T G A C G C C A G G G G C C A C G G G G A G A C T T C C T C A C A C C A A C T A C C C C A A G T	635
QY		1027	A C A A G C T T A G T G T A T G C C A G A C A C A C A T G T A G A G A T T A C C A C A G T G G G C C C C	1086
Dd		636	A C A A G C T T A G T G T A T G C C A G A C A C A C A T G T A G A G A T T A C C A C A G T G G G C C C C	695
QY		1087	A C T C C T G C A C A T C C C C A A G A C C T G G T C T C T T T A G C C C T A T A G A T C T G G T G A G G	1146
Dd		696	A C T C C T G C A C A T C C C C A A G A C C T G G T C T C T T T A G C C C T A T A G A T C T G G T G A G G	755
QY		1147	C C A C C A A C C G C T G G C T G C C C G C T C C G A T A C T A C A C C T G A A T A T C C T G A T G A G	1206
Dd		756	C C A C C A A C C G C T G G C T G C C C G C T C C A T A T A C T A C A C C T G A T A T C C T G A T G A G	815
QY		1207	T G A C C A G A A C C C C C G C C G A C G T G A C G T A G C C G C G T G G G G C C C T G A G A C A G C	1266
Dd		816	T G A C C A G A A C C C C C G C C G A C G T G A C G T A G A C C G G T G G G G C C C T G A G A C A G C	875
QY		1267	T G A G G G T G C G T G A G T G T G C C A C C G C C C T C A A G A T T T C C T T T C A A C C A A A T A T C	1326
Dd		876	T G A G C G T G C G T G A G T G T G C C A C C G C C C T C A A G A T T T C C T T T C A A C C A A A T A T C	935

QY	1327	AGATCCGCTACCGAGTGGAGGACAGTGTGACCTGAAAGTGTGAGACGATGTGACCAAC	1386
Db	936	AGATCCGCTACCGAGTGGAGGACAGTGTGACCTGAAAGTGTGAGACGATGTGACCAAC	995
QY	1387	AGACCTCTCTGCGGCTGTGGCCGCGCTGTAAACCCTGGACACGCTGTACTTGTGTGCAATGTGCGCT	1446
Db	996	AGACCTCTCTGCGGCTGTGGCCGCGCTGTAAACCCTGGACACGCTGTACTTGTGTGCAATGTGCGCT	1055
QY	1447	GCAACCCCTTTGGCATCTATGTGCTTCCAAAGAAAGCCGGGATCTTGGAGTGTGAGCCAC	1506
Db	1056	GCAACCCCTTTGGCATCTATGTGCTTCCAAAGAAAGCCGGGATCTTGGAGTGTGAGCCAC	1115
QY	1507	CCACAGCGCCCTCCACATCCCGGCGAGTGGGCGCCGGGCGCGGGGCGGGGCGGCGAC	1566
Db	1116	CCACAGCGCCCTCCACATCCCGGCGAGTGGGCGCCGGGCGCGGGGCGGGGCGGCGAC	1175
QY	1567	CGCGGGGCGAGAGACCGAGCTCGGGGGCGGAGTGGGCGCGAGCTTCAGCATGTTCTTGGGCT	1626
Db	1176	CGCGGGGCGAGAGACCGAGCTCGGGGGCGGAGTGGGCGCGAGCTTCAGCATGTTCTTGGGCT	1235
QY	1627	GGCTTCAGAGACAGCGCTTATGTGCTTCCAACTCTCAGCTTCCGCTCTTACGACAGTGTGGAG	1686
Db	1236	GGCTTCAGAGACAGCGCTTATGTGCTTCCAACTCTCAGCTTCCGCTCTTACGACAGTGTGGAG	1295
QY	1687	CCTGAGATCGAAGATGTGCAACAAGACCGGCAACAAGACGAGGGGATCTGCGCTCGGGCA	1746
Db	1296	CCTGAGATCGAAGATGTGCAACAAGACCGGCAACAAGACGAGGGGATCTGCGCTCGGGCA	1355
QY	1747	GACGGGACGCGGAGAGGTCTTGCAGATTAAGCTGTAGGGGCTCAGGGCAACCTCTCGTG	1806
Db	1356	GACGGGACGCGGAGAGGTCTTGCAGATTAAGCTGTAGGGGCTCAGGGCAACCTCTCGTG	1415
QY	1807	CCAGTGTGAGACGAGAGAGCCGGAACCCAACTGGGGCAACTCTGTATCCTCACTTACAG	1866
Db	1416	CCAGTGTGAGACGAGAGAGCCGGAACCCAACTGGGGCAACTCTGTATCCTCACTTACAG	1475
QY	1867	GCACCTTAGGCAACCTCAGACGAGAGCTGGGGTGGCCCTGTAGCTCCAACGGCATAACAG	1926
Db	1476	GCACCTTAGGCAACCTCAGACGAGAGCTGGGGTGGCCCTGTAGCTCCAACGGCATAACAG	1535
QY	1927	CTGTGACTCCACGTCGAGGCCACTTTTGGGTGACCCCACTGGGTGTGTGTGTGTGTG	1986
Db	1536	CTGTGACTCCACGTCGAGGCCACTTTTGGGTGACCCCACTGGGTGTGTGTGTGTGTGTG	1595
QY	1987	AGGGTGTGTGAGTGTGCTTGAATCCCTGACAGGGGCTGGGGGTGTGAGAAAGGGGATCATTA	2046
Db	1596	AGGGTGTGTGAGTGTGCTTGAATCCCTGACAGGGGCTGGGGGTGTGAGAAAGGGGATCATTA	1655
QY	2047	CTCCCACTTACCTTAGGGCCCTCCAAAGA	2076
Db	1656	CTCCCACTTACCTTAGGGCCCTCCAAAGA	1685
RESULT 6			
US-10-450-826-56			
Sequence 56, Application US/10450826			
Publication No. US20040101818A1			
GENERAL INFORMATION:			
APPLICANT: JI, Darren			
APPLICANT: Axelrod, Douglas W.			
APPLICANT: Cook, Jonathan S.			
APPLICANT: Jaiswal, Neelam			
APPLICANT: Eistein, Richard			
APPLICANT: Houghton, Adam			
APPLICANT: Mentz, Lawrence			
TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiation			
FILE REFERENCE: 044921-5039-WO			
CURRENT APPLICATION NUMBER: US/10/450,826			
CURRENT FILING DATE: 2003-06-18			
PRIOR APPLICATION NUMBER: US 60/255,882			
PRIOR FILING DATE: 2000-12-18			
PRIOR APPLICATION NUMBER: US 60/285,691			

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US-RSULT 6
US-10-450-826-56
Sequence 56, Application US/10450826
Publication NO. US2004010181
GENERAL INFORMATION:
APPLICANT: Ji, Darren
APPLICANT: Axelrod, Douglas W.
APPLICANT: Cook, Jonathan S.
APPLICANT: Jaiswal, Neilam
APPLICANT: Eistein, Richard
APPLICANT: Houghton, Adam
APPLICANT: Metzt, Lawrence
TITLE OF INVENTION: Gene Expression Profil
FILE REFERENCE: 044921-5039-WO
CURRENT APPLICATION NUMBER: US/10/450, 826
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/255, 882
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/285, 691

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1  TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiation
2  FILE REFERENCE: 044921-5039-WO
3  CURRENT APPLICATION NUMBER: US/10/450,826
4  CURRENT FILING DATE: 2003-06-18
5  PRIOR APPLICATION NUMBER: US 60/255,882
6  PRIOR FILING DATE: 2000-12-18
7  PRIOR APPLICATION NUMBER: US 60/285,691

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1 TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOT
2 FILE REFERENCE: P2548P1C1
3 CURRENT APPLICATION NUMBER: US/09/944,449
4 PRIOR FILING DATE: 2001-09-26
5 PRIOR APPLICATION NUMBER: 09/866,028
6 PRIOR FILING DATE: 2001-05-25
7 PRIOR APPLICATION NUMBER: 60/067,411
8 PRIOR FILING DATE: December 3, 1997
9 PRIOR APPLICATION NUMBER: 60/069,334
10 PRIOR FILING DATE: December 11, 1997
11 PRIOR APPLICATION NUMBER: 60/069,335
12 PRIOR FILING DATE: December 11, 1997
13 PRIOR APPLICATION NUMBER: 60/069,278
14 PRIOR FILING DATE: December 11, 1997
15 PRIOR APPLICATION NUMBER: 60/069,425
16 PRIOR FILING DATE: December 12, 1997
17 PRIOR APPLICATION NUMBER: 60/069,696
18 PRIOR FILING DATE: December 16, 1997
19 PRIOR APPLICATION NUMBER: 60/069,694
20 PRIOR FILING DATE: December 16, 1997
21 PRIOR APPLICATION NUMBER: 60/069,702
22 PRIOR FILING DATE: December 16, 1997
23 PRIOR APPLICATION NUMBER: 60/069,870
24 PRIOR FILING DATE: December 17, 1997
25 PRIOR APPLICATION NUMBER: 60/069,873
26 PRIOR FILING DATE: December 17, 1997
27 PRIOR APPLICATION NUMBER: 60/068,017
28 PRIOR FILING DATE: December 18, 1997
29 PRIOR APPLICATION NUMBER: 60/070,440
30 PRIOR FILING DATE: January 5, 1998
31 PRIOR APPLICATION NUMBER: 60/074,086
32 PRIOR FILING DATE: February 9, 1998
33 PRIOR APPLICATION NUMBER: 60/074,092
34 PRIOR FILING DATE: February 9, 1998
35 PRIOR APPLICATION NUMBER: 60/075,945
36 PRIOR FILING DATE: February 25, 1998
37 PRIOR APPLICATION NUMBER: 60/112,850
38 PRIOR FILING DATE: December 16, 1998
39 PRIOR APPLICATION NUMBER: 60/113,296
40 PRIOR FILING DATE: December 22, 1998
41 PRIOR APPLICATION NUMBER: 60/146,222
42 PRIOR FILING DATE: July 28, 1999
43 PRIOR APPLICATION NUMBER: PCT/US98/19330
44 PRIOR FILING DATE: September 16, 1998
45 PRIOR APPLICATION NUMBER: PCT/US98/25108
46 PRIOR FILING DATE: December 1, 1998
47 PRIOR APPLICATION NUMBER: 09/216,021
48 PRIOR FILING DATE: December 16, 1998
49 PRIOR APPLICATION NUMBER: 09/218,517
50 PRIOR FILING DATE: December 22, 1998
51 PRIOR APPLICATION NUMBER: 09/254,311
52 PRIOR FILING DATE: March 3, 1999
53 PRIOR APPLICATION NUMBER: PCT/US99/12252
54 PRIOR FILING DATE: June 22, 1999
55 PRIOR APPLICATION NUMBER: PCT/US99/21090
56 PRIOR FILING DATE: September 15, 1999
57 PRIOR APPLICATION NUMBER: PCT/US99/28409
58 PRIOR FILING DATE: No. US20020102647a1ember 30, 1999
59 PRIOR APPLICATION NUMBER: PCT/US99/28313
60 PRIOR FILING DATE: No. US20020102647a1ember 30, 1999
61 PRIOR APPLICATION NUMBER: PCT/US99/28301
62 PRIOR FILING DATE: December 1, 1999
63 PRIOR APPLICATION NUMBER: PCT/US99/30095
64 PRIOR FILING DATE: December 16, 1999
65 PRIOR APPLICATION NUMBER: PCT/US00/03565
66 PRIOR FILING DATE: February 11, 2000
67 PRIOR APPLICATION NUMBER: PCT/US00/04414
68 PRIOR FILING DATE: February 22, 2000
69 PRIOR APPLICATION NUMBER: PCT/US00/05841
70 PRIOR FILING DATE: March 2, 2000
71 PRIOR APPLICATION NUMBER: PCT/US00/08439
72 PRIOR FILING DATE: March 30, 2000

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[illegible]

Db 876 TGAGGCTGGGCTGGGTGGCCACCGCCCTCAAGGATTTCTTTCAAGCCAAATACC 935
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Db 936 AGATCCGCTACCGAGTGGAGGACAGTGTGACTGGAAAGTGGTGGACGATGTGAGCAACC 995
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Db 1176 CGGCGGGCGGAGAGCCGAGCTCGGGGCGGGTGCAGGCTCAAGCAGTTCTGGGCT 1235
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Qy 1687 CCTGATGCAAGAGTGGCACACACCCGCAACCAAGACGAGGGGATCTTGGCTCGGGCA 1746
Db 1296 CCTGATGCAAGAGTGGCACACACCCGCAACCAAGACGAGGGGATCTTGGCTCGGGCA 1355
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Db 1416 CCACGTGAGACACGACAGAGGCCAACCCAACTGGGGCAACCTTGTATCCTCACTTCAAG 1475
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Db 1536 CTCTGACTCCCACTGAGAGCCACTTTGGGTGACACCCAGTGGGTGTGTGTGTGTGTG 1595
Qy 1987 AGGGTGTGTTAGTTGCTTGAACCCCTGTCAGAGGCTGGGGGTGAAGAGGGGAGTCATTA 2046
Db 1596 AGGGTGTGTTAGTTGCTTGAACCCCTGTCAGAGGCTGGGGGTGAAGAGGGGAGTCATTA 1655
Qy 2047 CTCTCCATTACCTTGAAGGGCCCTTCCAAAAGA 2076
Db 1656 CTCTCCATTACCTTGAAGGGCCCTTCCAAAAGA 1685

RESULT 9
US-09-944-457-31
Sequence 31, Application US/09944457

GENERAL INFORMATION:
PATENT No. US20020110859A1
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerlitsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary

APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
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PRIOR FILING DATE: December 11, 1997
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PRIOR APPLICATION NUMBER: 60/069,696
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PRIOR APPLICATION NUMBER: 60/069,694
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PRIOR APPLICATION NUMBER: 60/069,873
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PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
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PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020110859A1member 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020110859A1member 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841

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 Db 816 TGACACGAGACCCCGCGCGAGCTGACAGTGAGCCGCTGGGGGCTTGAAGACAG 875
 Qy 1267 TGAGCGTGGCTGGGTGTGCGCAACCGCGCTCAAGATTTCTTTCAAGCAAAATACC 1326
 Db 876 TGAGCGTGGCTGGGTGTGCGCAACCGCGCTCAAGATTTCTTTCAAGCAAAATACC 935
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 Db 936 AGATCCGCTACCGAGTGAGAGAGTGTGATCTGGAAGGTGTGAGAGTGTGAGCAAC 995
 Qy 1387 AGATCTCTGCGCGCTGCGCGCTGAAACCCGCGCAACCGTGTACTTCTGCAAGTGCGCT 1446
 Db 996 AGATCTCTGCGCGCTGCGCGCTGAAACCCGCGCAACCGTGTACTTCTGCAAGTGCGCT 1055
 Qy 1447 GCAACCCCTTTGGATCTATGTGCTCAAGAAACCCGGAATCTGAGTGAAGTGAAC 1506
 Db 1056 GCAACCCCTTTGGATCTATGTGCTCAAGAAACCCGGAATCTGAGTGAAGTGAAC 1115
 Qy 1507 CCAACCGCTCTCACTCCCGGAGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGTGAAC 1566
 Db 1116 CCAACCGCTCTCACTCCCGGAGTGAGCGCGCGCGCGCGCGCGCGCGCGCGTGAAC 1175
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 Db 1176 CGCGGGGCGGAGAGCGGAGCTCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 1235
 Qy 1627 GGTCTAAGAAAGCAAGGTAATGCTCAACTCACTTCCGCTCTTCAAGCAAGTGGGAG 1686
 Db 1236 GGTCTAAGAAAGCAAGGTAATGCTCAACTCACTTCCGCTCTTCAAGCAAGTGGGAG 1295
 Qy 1687 CCGGATGCAAGAGTGGCAACCAACCGCAACCAAGCAAGGAGATCTGCGCGGCA 1746
 Db 1296 CCGGATGCAAGAGTGGCAACCAACCGCAACCAAGCAAGGAGATCTGCGCGGCA 1355
 Qy 1747 GACGGGGGCAAGGAGAGTCTGCAAGATTAAGTGAAGGAGTCAAGGCAACCTCGCTG 1806
 Db 1356 GACGGGGGCAAGGAGAGTCTGCAAGATTAAGTGAAGGAGTCAAGGCAACCTCGCTG 1415
 Qy 1807 CCAAGTGAGAGAGCAAGAGCGCAACCAACCAAGTGAAGTGAAGTGAAGTGAAG 1866
 Db 1416 CCAAGTGAGAGAGCAAGAGCGCAACCAACCAAGTGAAGTGAAGTGAAGTGAAG 1475
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 Db 1476 GCAACGAGAGCAACCTCAGAGAGAGTGGGCTGAGCTCAACGAGCAATTAACAG 1535
 Qy 1927 CTCTGACTCCAGTGAAGGCACTTTGGGTGCAACCAAGTGGGTGTGTGTGTGTG 1986
 Db 1536 CTCTGACTCCAGTGAAGGCACTTTGGGTGCAACCAAGTGGGTGTGTGTGTGTG 1595
 Qy 1987 AGGTTGGTTGAGTGTGCTGAAGACCCCTGCAAGGCTGGGGGTGAAGAGGAGTCA 2046
 Db 1596 AGGTTGGTTGAGTGTGCTGAAGACCCCTGCAAGGCTGGGGGTGAAGAGGAGTCA 1655
 Qy 2047 CTCCTCATTAACCTAAGGCGCTCAAGAGA 2076
 Db 1656 CTCCTCATTAACCTAAGGCGCTCAAGAGA 1685

RESULT 13
 US-09-944-432-31
 ; Sequence 31, Application US/09944432
 ; Patent No. US20020142419A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David
 ; APPLICANT: Baton, Dan
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerltisen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Hillen, Kenneth
 ; APPLICANT: Kljavin, Ivar
 ; APPLICANT: Napier, Mary
 ; APPLICANT: Roy, Margaret
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P2548P1C1
 ; CURRENT APPLICATION NUMBER: US/09/944,432
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 09/866,028
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/067,411
 ; PRIOR FILING DATE: December 3, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,334
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,335
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,278
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,425
 ; PRIOR FILING DATE: December 12, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,696
 ; PRIOR FILING DATE: December 15, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,694
 ; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,702
 ; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,870
 ; PRIOR FILING DATE: December 17, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,873
 ; PRIOR FILING DATE: December 17, 1997
 ; PRIOR APPLICATION NUMBER: 60/068,017
 ; PRIOR FILING DATE: December 18, 1997
 ; PRIOR APPLICATION NUMBER: 60/070,440
 ; PRIOR FILING DATE: January 5, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,086
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,092
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/075,945
 ; PRIOR FILING DATE: February 25, 1998
 ; PRIOR APPLICATION NUMBER: 60/112,850
 ; PRIOR FILING DATE: December 16, 1998
 ; PRIOR APPLICATION NUMBER: 60/113,296
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 60/146,222
 ; PRIOR FILING DATE: July 28, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US98/19330
 ; PRIOR FILING DATE: September 16, 1998
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108
 ; PRIOR FILING DATE: December 1, 1998
 ; PRIOR APPLICATION NUMBER: 09/218,517
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 09/254,311
 ; PRIOR FILING DATE: March 3, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252
 ; PRIOR FILING DATE: June 22, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: September 15, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28409

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DB 636 ACAGCTTAGGTGATGCGCAGAGCAACATGTGAGAGTACACAGATGGGGCCCC 695
QY 1087 ACTCTGCGCATCTCCCAAGAACTGGCTCTTTTACGCCCTATGAGATCTGGGTGAGG 1146
DB 696 ACTCTGCGCATCTCCCAAGAACTGGCTCTTTTACGCCCTATGAGATCTGGGTGAGG 755
QY 1147 CCAACCAAGCGGCTGGGGCTGGCCGCTCCATGTACTCAGCGTGGATATCTGGATGTGG 1206
DB 756 CCAACCAAGCGGCTGGGGCTGGCCGCTCCATGTACTCAGCGTGGATATCTGGATGTGG 815
QY 1207 TGAACACGACCCCGCCCGCAGCTGACGTCGACCGCGCTCGAGGGGCTGAGAGACGAGC 1266
DB 816 TGAACACGACCCCGCCCGCAGCTGACGTCGACCGCGCTCGAGGGGCTGAGAGACGAGC 875
QY 1267 TGAAGCTGCGCTGGGTGTGCGCACCGCGCTCAAGAGATTTCTCTTCAAGCCAAATACC 1326
DB 876 TGAAGCTGCGCTGGGTGTGCGCACCGCGCTCAAGAGATTTCTCTTCAAGCCAAATACC 935
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DB 936 AGATCCGCTACCGAGTGAAGAGACAGTGTGAGCTGGAAGGTGTGGAAGATGTGAGCAAC 995
QY 1387 AGACCTCTCGCGCTGGCGCTGGAACCCGGCACCCTGTACTTCTGTCAAGTGGCT 1446
DB 996 AGACCTCTCGCGCTGGCGCTGGAACCCGGCACCCTGTACTTCTGTCAAGTGGCT 1055
QY 1447 GCAACCCCTTTGGCATCTATGCTCAAGAAAGCCGGGATCTGAGTGTGAGTGAAGCCACC 1506
DB 1056 GCAACCCCTTTGGCATCTATGCTCAAGAAAGCCGGGATCTGAGTGTGAGTGAAGCCACC 1115
QY 1507 CCAACCGCGCTCACTCCCCGAGTGAAGGCGCCGGGCGGGGGGGGGGGGGGGGCAAC 1566
DB 1116 CCAACCGCGCTCACTCCCCGAGTGAAGGCGCCGGGCGGGGGGGGGGGGGGGGCAAC 1175
QY 1567 CGCGGGGCGGAGAGCCAGCTCGGGGCGGGTGCAGGCTCAAGCAGTTCCTGGGCT 1626
DB 1176 CGCGGGGCGGAGAGCCAGCTCGGGGCGGGTGCAGGCTCAAGCAGTTCCTGGGCT 1235
QY 1627 GGGTCAAGAGACCGCTACTGTCTCAACCTCAAGCTTCGCGCTTACAGCAGTGGCGAG 1686
DB 1236 GGGTCAAGAGACCGCTACTGTCTCAACCTCAAGCTTCGCGCTTACAGCAGTGGCGAG 1295
QY 1687 CCTGATGACGAGTGTGCAACAGCCCGCAACAGAGCAGGGGATCTGCGCTCGGGCA 1746
DB 1296 CCTGATGACGAGTGTGCAACAGCCCGCAACAGAGCAGGGGATCTGCGCTCGGGCA 1355
QY 1747 GACGGGGCAGCGGAGAGTCTGCGCAGATAGCTGAGGGGCTCAGGCCACCTCCCTG 1806
DB 1356 GACGGGGCAGCGGAGAGTCTGCGCAGATAGCTGAGGGGCTCAGGCCACCTCCCTG 1415
QY 1807 CCAAGTGAAGACGCAAGGCGCAACCCAACTGGGGGCACTCTGTACCTCACTTCAGG 1866
DB 1416 CCAAGTGAAGACGCAAGGCGCAACCCAACTGGGGGCACTCTGTACCTCACTTCAGG 1475
QY 1867 GCACTGAGAGCACTCTCAGAGAGAGTGGGGTGGCCCTTGAAGTCCCAAGCCCAATACAG 1926
DB 1476 GCACTGAGAGCACTCTCAGAGAGAGTGGGGTGGCCCTTGAAGTCCCAAGCCCAATACAG 1535
QY 1927 CTCTGACTCCCACTGAGGCACTTTGGGTGACCCCACTGGGGTGTGTGTGTGTGTG 1986
DB 1536 CTCTGACTCCCACTGAGGCACTTTGGGTGACCCCACTGGGGTGTGTGTGTGTGTG 1595
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DB 1596 AGGGTGTGTTGAGTGTGCTTGAACCCCTGCGCAGGGGCTGAGGGGTGAGAGGGGAGTCAATTA 1555
QY 2047 CTCCTCATTAACCTTAAAGGCGCCCTCCAAAAGA 2076
DB 1656 CTCCTCATTAACCTTAAAGGCGCCCTCCAAAAGA 1685

RESULT 15
US-09-944-654-31
Sequence 31. Application US/09944654
Patent No. US20020142959A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Geriltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Christopher
APPLICANT: Guirney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: KJavian, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,654
CURRENT FILING DATE: 2001-09-26
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PRIOR APPLICATION NUMBER: 60/069,278
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PRIOR APPLICATION NUMBER: 60/070,440
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PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
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PRIOR APPLICATION NUMBER: 60/146,222
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PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311

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